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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Match Length
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfIles1.pep:*
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SUMMARIES
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               Sequence 22, Appl
Sequence 1, Appli
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22
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US-09-778-510-22
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APPLICANT:

TITLE OF INVENTION:

PLIE REFERENCE:

PLIE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/778,510

CURRENT FILING DATE:

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:

PRIOR F
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SOFTWARE: Patentin Ver.
SEQ ID NO 22
LENGTH: 423
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Patent No. 6512095
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                                             VGKAHSDYMLYVYDPPTTTIPPPTTTTTTTTTTTTTLTITITTILTIGSRAGEEGTIGAVDHAVIG
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US-09-614-124B-334
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US-09-691-325-34
US-09-691-4657D-47
US-08-414-657D-42
US-08-414-657D-42
US-08-414-657D-43
US-08-17-299-1
US-08-207-725-36
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US-08-207-725-36
US-08-207-725-36
US-08-207-725-36
US-08-207-725-36
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US-08-98-684-594-2
US-08-98-6594-59
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Result

Score 2197

Length 423; Indels

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Gaps

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240

360 300 300 2

2169 2149 2149 904 893.5 893.5 732.5

Database

Minimum DB Maximum DB

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length:

ALIGNMENTS

Sequence 4, Appli Sequence 34, App Sequence 334, App Sequence 334, App Sequence 334, App Sequence 42, Appli Sequence 42, Appli Sequence 4, Appli Sequence 4, Appli Sequence 17, Appli Sequence 17, Appli Sequence 27, Appli Sequence 23, Appli Sequence 231, Appli Sequence 531, Appli Sequence 531, Appli

Scoring table: Sequence: Title: Perfect score:

BLOSUM62

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; Sequence 1, Application US/09930803; Patent No. 6596493; GENERAL INFORMATION:
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US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
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Baum, Peter
TITLE OF INVENTION:
FILE REFERENCE:
2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION UNMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/995,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
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SEQ ID NO 20
LENGTH: 442
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Matches 418
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98.8%; Pred. No. 1.2e-184;
ltive 1; Mismatches 4; Indels
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; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: VOSHINDA; MUTAMAKİ
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSO
; FILE REFERENCE: JHU1770-1
; CURRENT APPLICATION UNUMBER: US/09/930,803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTMARE: Patentin version 3.0
; SBQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
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RESULT 4 US-09-866-028-61 GENERAL INFORMATION:
APPLICANT: Baker, K
APPLICANT: Botstei APPLICANT:
APPLICANT:
APPLICANT: Sequence 61, Appli Patent No. 6642360 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Gerritsen, Mary Goddard, Audrey Godowski, Paul Grimaldi, Christopher Gurney, Austin Hillan, Kenneth Ferrara, Napoleone Filvaroff, Ellen Wood, William Napier, Mary Roy, Margaret Eaton, Dan Botstein, David Application US/09866028 Tumas, Danie Kljavin, Ivar Kevin

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Best Local S
Matches 416
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SEQ ID NO 61 LENGTH: 440 TYPE: PRT ORGANISM: Homo Sapien ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                              Sequence 5, Application US/08659984A Patent No. 5942400 GENERAL INFORMATION:
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                  APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten
TITLE OF INVENTION: Assays for Dete
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
STREET: Two Embarcadero
                                                                                                           CITY: San Francisco
STATE: California
                                                                                           COUNTRY:
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416; Conserv
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                                                                                                                                          Townsend a
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Pred. No. 7.
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      Version
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7.2e-183;
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Sequence 5, Application US/08660531

Patent No. 6221645

GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.

Chrysler, Susanna M.S Sinha, Sukanto

APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

and

RESULT 6 US-08-660-531-5

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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Heslin, James M. REGISTRATION NUMBER: 29, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01
FILING DATE: 07-JUN-1996
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                                                                                                                                                            ILTCESKGKPLPEPVLWTKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCEATNTIGQ
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                                                                                                                                 SSAEYVLIVHDVPNTLLPTTIIPSLTTATVTTTVAITTSPTTSATTSSIRDPNALAGQNG
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                                                                                                                                                                                                                                                                                                                                                                                                    DKKALRDNRIELVRASWHELSISVSDVSLSDEGQYTCSLFTMPVKTSKAYLTVLGVPEKP 136
EGSQVNAEEKKEYF
                                 EGGQNNSEEKKEYF
                                                                  P----DHALIGGIVAVVVFVTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINA
                                                                                                TIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINA 409
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44.7%;
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Pred. No. 4.2e-72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 444;
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313 303 253 245

349 373

STATE: C. STREET:

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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIA Release #1.0, Version #
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/480,498
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELEPHONE: 415-226-2400
TELEPHONE: 415-226-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                           304 AHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTILTIIT-------DSRAGEEG 349
                                                                                                                                                                                                                                                                                                                                                                                                                    246 ELTCEAIGKPQPVMVTWVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGK 303
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           Application US/08659984A
                                                                                                                                                                                                           P----DHALIGGIVAVVVFVTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINA
                                                                                                                                                                                                                                                                                                SSAEYVLIVHDVPNTLLPTTIIPSLTTATVTTTVAITTSPTTSATTSSIRDPNALAGONG
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California
                                                                                                                                                                EGGQNNSEEKKEYF
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ilarity 44.7%;
Conservative 7
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Pred. No. 4.2e-72;
4; Mismatches 136
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GENERAL INFORMATION:
APPLICANT: Anderso
APPLICANT: Sinha,
APPLICANT: Jacobso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.7%; Score 893.5; DB 2; Best Local Similarity 45.0%; Pred. No. 3.3e-71; Matches 188; Conservative 73; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILLING DATE: 07-7UN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
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FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting
TITLE OF INVENTION: Inhibition
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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366 VVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKKEYF
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                                                                    LPTTIIPSLTTATVTTTVAITTSPTTSATTSSIRDPNALAGONGP----DHALIGGIVAV
                                                                                                        PPPTTTTTTTTTTILTIIT------DSRAGEEGTIGAVDHAVIGGVVAV
                                                                                                                                                         WTKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCEATNTIGQSSAEYVLIVHDVPNTL
                                                                                                                                                                                               WVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCBASNIVGKAHSDYMLYVYDPPTTI 319
                                                                                                                                                                                                                                                 RVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPFPQEGQPLILTCESKGKPLPEPVL
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RESULT 7 US-08-659-984A-1

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US-08-660-531-5

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Matches Query Match

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Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysl
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Best Local S
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 421 amino
TYPE: amino acid
STRANDEDNESS: sinc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                  WTKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCEATNTIGQSSAEYVLIVHDVPNTL
                                                 WVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTI
                                                                                   RVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPPPQEGQPLILTCESKGKPLPEPVL
                                                                                                                    QVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVT
                                                                                                                                                       LTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSTLDFRVDRSDDGVAVIC
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Keim, Pamela S.
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45.0%; Pred. No. 3.3e-71
7ative 73; Mismatches 13
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Sequence 6, Application US/09778510 Patent No. 6512095 GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver.
SEQ ID NO 4
LENGTH: 398
TYPE: PRT
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PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 19:
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CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baum, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                           SNMGSYTAYFTLNVNDPS---PVPSSSSTY----
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                                                                                                                      KKEYF
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Pred. No. 1.9e-57;
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US-09-907-794A-84
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LENGTH: 398
TYPE: PRT
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Best Local
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CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/179
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
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                                 APPLICANT
                                                                                                                                                                                APPLICANT: Genentech, APPLICANT: Ashkenazi, APPLICANT: Botstein,
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                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity 38.3
162; Conservative
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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                                                                                                                                                                                Benentech, Inc.
Ashkenazi, Avi
Botstein, David
                                                                                                              Ferrara, Na
Filvaroff,
Grimaldi,
            Godowski,
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Eaton, Dan L.
                                 Goddard, A.
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f, Ellen
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Molecules Designated
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Paul J.
Christopher
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PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR APPLICATION NUMBER: PCT/US99/21547
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Best Local S
Matches 162
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PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
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FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
APPLICATION NUMBER: PCT/US99/30999
FILING DATE: 1999-12-20
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FILING DATE: 1999-12-02
APPLICATION NUMBER: PCT/US99/28565
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
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FILING DATE: 1999-11-30
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                                                                                                                                                                                                                                           al Similarity
162; Conserv
129 IPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTF 188
                                     125 PPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGK-SEVEEWSD--MY
                                                                          10 LLLLLLSAAALIPTG-----DGONLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQ
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THE WOOD, WILLIAM, I.
THE WOOD, WILLIAM, I.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
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                                                                                                                                                                                                                                           33.3%; Score 732.5; DB 4; ilarity 38.3%; Pred. No. 6.5e-57; Conservative 74; Mismatches 144;
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                                                                                                                                                                                                                                                                                     Length 398;
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APPLICANT: Williams, Dullet
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR PPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: DCT/US99/20594
PRIOR APPLICATION NUMBER: DCT/US99/20944
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US-09-905-125A-84
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Patent No.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
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                     APPLICATION NUMBER: PCT/US99/21547 FILING DATE: 1999-09-15
                                                         FILING DATE: 1999-09-15
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5. 6664376
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Gao, Wei-Qiang
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
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Tumas, Daniel
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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Mather, Jennie P.
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Grimaldi, Christopher
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Filvaroff, Ellen
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art, Timothy A.
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       PCT/US99/23089
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                                                                                       RESULT 13
US-09-902-775A-84
; Sequence 84, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
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Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
PTYPE: PRI
CECANISM. HOWO CERNICAE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 PPRNLMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGK-SEVEEWSD--MY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LILLLISAAALIPTG-----DGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQ
                                                                  GVVAVVVFAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGONNSEEKK
                                                                                                                                                                                                                   VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTLTIITDSRAGEEGIIGAVDHAVIG
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GIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDDAPDADTAIINAEGGOSGGDDKK
                                                                                                                                             MGSYKAYYTLNVNDPS---PVPSSSSTY----
                                                                                                                                                                                                                                                                                          EGOKLLIHCEGRGNPVPQQYLWEK-EGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                       TVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPP---HPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVTSQLMLKVHKEDPGVPVICQVEHPAVTG-NLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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Pred. No. 6.5e-57;
4; Mismatches 144;
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SEQ ID NO 84
LENGTH: 398
                                                                                                                            Matches
                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14 CURRENT APPLICATION NUMBER: US/09/902,775A CURRENT FILING.DATE: 2001-07-10 PRIOR APPLICATION NUMBER: PCT/US00/04414 PRIOR APPLICATION NUMBER: US/09/902,075A PRIOR PILING DATE: 2000-02-22 PRIOR APPLICATION NUMBER: US/09/902,075A PRIOR PILING DATE: 1099-07-07 PRIOR PILING DATE: 1099-07-07 PRIOR FILING DATE: 11999-07-07
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PRIOR FILING DATE: 1999-09-13
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PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
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FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/28564
FILING DATE: 1999-12-02
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FILING DATE: 1999-11-29
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APPLICATION NUMBER: PCT/US99/23089
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FILING DATE: 1999-09-08
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FILING DATE: 1999-12-02
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                                                                               10 LILLLISAAALIPTG-----DGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNENRQ
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TIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLV 124
                                          LLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWSNPAQQ
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Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fong, buccang
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Mather, Jennie P.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
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                                                                                                                            Conservative
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                                                                                                                     33.3%; Score 732.5; DB 4; 38.3%; Pred. No. 6.5e-57; tive 74; Mismatches 144;
                                                                                                                                                                  Length
                                                                                                                            Indels
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2
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US-09-778-510-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                           Matches 165;
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/179
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
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                                                          189
                                                                                          151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 IPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 PPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGK-SEVEEWSD--MY
249
                        208 AVTG-NLQTQRYLEYQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVD
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                                                                                      MASKPATTIRWFKGNKELKGK-SEVEEWSD--MYTVTSQLMLKVHKEDDGVPVICQVEHP
                                                                                                                       ISISNVALADEGEYTCSIFTMPVRTAKSLVTVLGIPQKPIITGYKSSLREKDTATLNCQS
                                                                                                                                              VSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTA
                                                                                                                                                                           TSDETVVAGGTVVLKCQVKDHEDSSLQWSNPAQQTLYFGEKRALRDNRIQLVTSTPHELS
                                                                                                                                                                                                    TXDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELK
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TLYFGEKRALRDNRIQLVTSTPHELSISISNVALADEGEYTCSIFTMPVRTAKSLVTVLG
SLKGADRSTSQRIEVLYTPTAMIRPDPP--
                                                         SGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFTVSSSVTFQVTREDDGASIVCSVNHE
                                                                                                                                                                                                                                               LLLLLFACCWAPGGANLSQDGYWQEQDLELGTLAPLDEAISSTVWSSPDMLASQDSQPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baum, Peter
                                                                                                                                                                                                                                                                                                        32.6%; Score 715.5; DB 4; 36.1%; Pred. No. 2.4e-55; tive 75; Mismatches 140;
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CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,901
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APPLICATION NUMBER: 60/048,892
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,899
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APPLICATION NUMBER: 60/048,971
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APPLICATION NUMBER: 60/048,896
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APPLICATION NUMBER: 60/048,972
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
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APPLICATION NUMBER: 60/048,916 FILING DATE: 1997-06-06
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; EARLIER FILING DATE: 1998-07-30; NUMBER OF SEQ ID NOS: 1227; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 947; LENGTH: 227; TYPE: PRT CRGANISM: Homo sapiens US-09-205-258-947
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EARLIER APPLICATION NUMBER: 60
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APPLICATION NUMBER: 60/048,898
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APPLICATION NUMBER: 60/048,974
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APPLICATION NUMBER: 60/049,374
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2283
1 MASVVLPSGSQCAA
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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ALIGNMENTS

TO8732 A;Molecule type: mRNA A;Residues: 1-407 <OTT> A;Cross-references: EMBL:AL050071 A;Experimental source: fetal kidney; clone DKFZp566B0846 A; Note: C; Genetics: A; Reference number: Z16474 A; Accession: T08732 R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999 hypothetical protein DKFZp566B0846.1 - C;Species: Homo sapiens (man) C;Date: 11-Uun-1999 #sequence_revision C;Accession: T08732 Query Match Best Local Similarity Matches DKFZp566B0846.1 343 286 233 173 291 115 120 GRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQXDTAVEG--ESIEVNCTAMASKPAT 175 231 LQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQH 176 TIRWFKGNTELKGKSEVEEWSDMY-----TVTSQLMLKVHKEDDGVPVICQVEHPAVTGN 230 61 84; 2 GKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLIDGGNETVAAICIAATGKPVA HIDW-EGDL-----GEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKD LASDNTLHEVHDLTENYSGYYICKVTNSLGQRSDQKVIYISDPTTTTLQFTIQMHPST YRRRRTFRGDYFAKN -----ILGRYFARH 402 ADIEDLATEPKKLPFPLSTLATI------KDDTIATIIASVVGGALFIVLVSVLAGIFC TTTTTTT-----TTTLTITDSRAGEEGS!RAVDHAVIGGVVAVVVFAMLCLLI-AVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPP--TTIPP----PTT IRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNADANPPPFKSVWSRLDGQWPDG Conservative 11.7%; 60; Score 268; DB 2; L Pred. No. 1.4e-11; 0; Mismatches 123; 11-Jun-1999 #text_change 13-Aug-1999 human (fragment) Length 407; Indels 48; Gaps 172 114 60 393 342

RESULT 2 T20992

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hypothetical protein F15G9.4a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T20992; T24733

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submitted to the EMBL Data Library, A;Reference number: Z19929 A;Accession: T24733 A;Status: preliminary.
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A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; A;Introns: 85/1; 269/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4251/2; 2593/3; 4361/1; 4408/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/
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A; Molecule type: DNA
A; Residues: 1-5175 <WILD
A; Cross-references: EMBL: Z47068; PIDN: CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
A; Cross-references: EMBL: Z47068; PIDN: CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
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A,Experimental source: clone T09B9
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A;Molecule type: DNA
A;Residues: 1-5175 <WIZ>
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submitted to the EMBL Data A; Reference number: Z19355 A; Accession: T20993
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                                                                       A, Molecule type: mRNA
A, Residues: 1-5198 < VOG>
A, Cross-references: EMBL
R, Sulston, J.
                                                                                                                                                                                                                 R;Vogel, B.E.; Hedgecock, E.M. submitted to the EMEL Data Library, June 1998 A;Description: Hemicentin is required for hemidesmosome mediated A;Reference number: Z22396
                                                                                                                                                                                                                                                                                                                                                             hemicentin precursor - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
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Matches 87
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1 Similarity 24.6%; Pred. No. 7.6e-10;
87; Conservative 66; Mismatches 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIGKPQPVMVTWVRVDDEMPQHAVL----SGPNLFINNLNKTDNGTYRCEASNIVGKAHS
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er: Z19355
                                                                                                 EMBL: AF074901; PIDN: AAC26792.1
                                                     Library,
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A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
E;1-30/Domain: signal sequence #status predicted <SIG>
F;31-518/Product: poliovirus receptor-related protein #status
E;356-379/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                       C;Accession: JC4024
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg,
Gene 155, 261-265, 1995
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A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; A;Introns: 85/1; 120/1; 334/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/
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A;Molecule type: DNA
A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL: Z47068; PIDN:CAA87336.1; G
                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
A;Cross-references: EMBL:X76400; NID:g732795;
                                                                                                                                                                                                                                                                                         A; Title: Complementary DNA characterization A; Reference number: JC4024; MUID:95237621; E
                                                                                                                                                                                                                                                                                                                                                                                                           pollovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
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A;Residues: 1-5198 <WI2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A;Reference number: Z19929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Kershaw,
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                                                                                                                                    A; Cross-references: GDB:583951
                                                                                                                                                       A;Gene: GDB:PVRR1
                                                                                                                                                                                    C;Genetic
                                                                                                                                                                                                                                                                      A; Accession: JC4024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 263.5; DB 2;
Pred. No. 7.6e-10;
6; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  December
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poliovirus receptor mPVR - mouse
(;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
C;Accession: A53437
R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involv
A;Reference number: A53437; MUID:94179228; PMID:8132589
A;Accession: A53437
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A;Molecule type: mRNA
A;Residues: 1-530 <AOK>
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Best Local S
Matches 91
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Best Local S
Matches 105
                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:D26107; NID:9475017; PIDN:BAA05103.1; Experimental source: C57/BL6, brain provided from NCBI backbone (NCBIN:146664, NOte: sequence extracted from NCBI backbone (NCBIN:146664, Superfamily: poliovirus receptor; immunoglobulin homology; 47-133/Domain: immunoglobulin homology < IMM>
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V------NCTAMASKPATTIRWEKG-NTELKGKSEVEEWSDMYTVTSQLMLKVHKEDD
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                                                          DATLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPEN------HAEAQEVT
                                                                                              ELKVSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQKDTAVEGEEIE
                                                                                                                                LPPTTERVSQVTWQRLDGTVVAAFHPS----FGVDFPNSQFSKDRLSFVRARPETNADLR
                                                                                                                                                                                                                                               AAAAAAPPG-----LRLRLLLLLESAAALIPTGDGQNLFTKDVTVIEGEV---ATISCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKHVYGNGYSKAGIPQHHPPMAQNLQYPDDSDDEKKA--GPLGGSSYEEEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQYEPEVTIEGFDGNWYLQRMD-----VKLTCKADANPPATEYHWTTLNGSLPKGVEAQN
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                                                                                                                                                                                                             ARAAVLPPSRLSPTLPLLPLLLL-----LLQETGAQDVRVRVLPEVRGRLGGTVELPCHL
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                                                                                                                                                                                                                                                                                                       10.8%;
                                                                                                                                                                    -NKSDDSVIQLENPNRQTIYFRDFRPLKDSRFQL-----LNFSSS
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                                                                                                                                                                                                                                                                               Score 247.5; DB 2;
Pred. No. 5.5e-10;
""Gmatches 166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       poliovirus receptor (clone AGM-alpha-1) - green monkey
C;Betes: Cercopithecus aethiops (green monkey, grivet)
C;Betes: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: A44194
R;Koike, S:; Ise, I:; Sato, Y:; Yonekawa, H:; Gotoh, O:; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has A;Reference number: A44194, MUID:93059651; PMID:1331508
A;Reference number: A44194, MUID:93059651; PMID:1331508
A;Recession: A44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-417 < KOI>
A;Cross-references: GB:548777
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology <IMM>
  RESULT
HLMSP3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDEGRYFCQLYTDPPQESYTT---ITVLVPPRNLMIDIQXDTAVEGEEIEV-NCTAMASK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEETHVSQLTWSRHGESGSMAVFHQTQGPNYSEPKRLEFVAARLGTELRDASLRMFGLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAAAAAPPGLRLRLLLLESAAALIPTGDGQNLFTKDVTV--IEGEVATISC--QVNK
                                                                              CSREFLWCHHLSPSSEEHASA - - -
                                                                                                              GT----YFTHEAKGADDAADADTAIINAEGGONNSEEKKE 439
                                                                                                                                                                                                                             PFÄVAQGAQLLIRPVDKPINTTFICNVTNALGARQAELTVQVKEGPPSEPSGMSSN----
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                                                                                                                                                                                      TTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIIL-----GRYFARHK
                                                                                                                                                                                                                                                                                                                                                                               PPAHITW---HSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTCKVEHESFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARTMAAAWPP-----LLITLLELSWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPG
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                                                                            -SANGYISYSDVSRE
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F;167-231/Domain: immunoglobulin homology <IMM2>
F;267-322/Domain: immunoglobulin homology <IMM3>
F;355-374/Domain: transmembrane #status predicted <TMN>
F;375-467/Domain: intracellular #status predicted <IMT>
F;375-467/Domain: intracellular #status predicted <IMT>
F;54-131,174-229,274-320/Disulfide bonds: #status predicted
F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status
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neural cell adhesion molecule 1 - African clawed frog
N;Alternate names: N-CAM 1
C;Species: Kenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0099
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAM A;Reference number: JE0099; MUID:98204770; PMID:9535795
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A; Residues: 1-467 < MOR>
A; Cross-references: GB: M80206; NID: g199785; PIDN: AAA39734.1;
A; Cross-references: GB: M80206; NID: g199785; PIDN: AAA3974.1;
A; M80206; PIDN: AAA3974; P
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J. Virol. 66, 2807-2813, 1992
A;Title: Molecular cloning and expression of a murine homolog
A;Reference number: A38211; MUID:92219365; PMID:1560525
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C;Species: Mus musculus domesticus (western European house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
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A; Residues: 1-46
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21.0%;
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Pred. No. 8.3e-10;
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A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g3116227
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through bo C;Commently: neural cell adhesion molecule; fibronectin type III repeat homology; immu F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>
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A,Residues: 1-538 <RES>
A,Cross-references: GB:S79172; NID:g1042204; PID:g1042205
                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #
C;Accession: I68093
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard,
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard,
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human pR71tle: The human PRR2 gene, related to the human pRR2 A;Tetce number: 153960, MUID:95347610; PMID:7622
A;Accession: I68093
A;Status: preliminary; translated from GB/EMBL/DDBJ
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F; 276-331/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 ISFNEDQSEMTIHHVEKDDEAEYSC-IANNQAGEAEATILLKVYAKPKITYVENKTAVEL
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                                                                                                                                                   10 SQCAAAAAAAAAPPGLRLRLLLLLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKS
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                                                                           DDSVIQLLNP-
                                                                                                                 ARAAALLPSRSPPTPLLWPLLLLL----LLETG-AQDVRVQVLPEVRG
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                                                                                                                                                                                                                                                                 poliovirus receptor; immunoglobulin homology
in: immunoglobulin homology <IMM>
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                                                                                                                                                                                         Conservative
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   ELKVSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMI
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                                                                                                                                                                                                           Score 242.5; DB 2
Pred. No. 1.3e-09;
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Pred. No. 1.7e-09
1; Mismatches 14
                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                             DB 2;
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A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
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C;Superfamily: poliovirus receptor; immunoglobulin
F;259-314/Domain: immunoglobulin homology <IVM>
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R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, J. Virol. 66, 7059-7066, 1992

A;Title: A second gene for the African green monkey poliovirus representations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
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A; Residues: 1-392 < KOI>
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                                                                                                                                                                                                 EDEGNYTC-LFVTFPQGSRSVDIWLRVLAKPQN-TAEVQK-VQLTGKPVPVARCVSTGGR
                                                                                                                                                                                                                           SDEGRYFCQLYTDPPQESYTT---ITVLVPPRNLMIDIQKDTAVEGEEIEV-NCTAMASK 172
                                                                                                                                                                                                                                                              MEETHVSQLTWSRHGESGSMAVFHQTQGPNYSEPKRLEFVAARLGTELRDASLRMFGLRV
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 PFAVAQGAQLLIRPVDKPINTTFICNVTNALGARQAELTVQVKEGPPSEPSGMSSN----
                             QHAVLSGBNLFINNLNKTDNGTYRCEASNI VGKAHSDYMLYVYDBPTTI PPPTTTTTTT
                                                              KPQLLTVNITVYYPPEVSIS-GYDNNWYLSQNEA-TLTCDARSNPEPTGYNWSTINGPLP
                                                                                                                                                                PATTIRWFKGNTELKGKSEVEE----WSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVT
                                                                                             GNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMP
                                                                                                                               PPAHITW---HSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTCKVEHESFE
                                                                                                                                                                                                                                                                                                                            ARTMAAAWPP-----LLLTLLELSWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPG
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            Score 241.5; DE 
Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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A; Cross-references: GDB:120324; OMIM:173850
A; Map position: 19q13.2-19q13.2
A; Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C; Superfamily: poliovirus receptor; immunoglobulin homology C; Keywords: alternative splicing; duplication; glycoprotein; r F; 1-20/Domain: signal sequence #status predicted <SIG-F; 21-392/Product: poliovirus receptor delta #status predicted F; 21-343/Domain: extracellular #status predicted <EXT-F; 159-223/Domain: immunoglobulin homology <IMM1>F; 159-223/Domain: immunoglobulin homology <IMM1>F; 159-233/Domain: immunoglobulin homology <IMM2>F; 259-314/Domain: immunoglobulin homology <IMM3>F; 259-314/Domain: immunoglobulin homology <IMM3-F; 259-3
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A;Title: Cellular receptor for poliovirus: A;Reference number: A90910; MUID:89168426; A;Accession: B31496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble C;Genetics:
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A;Residues: 1-66,'A',68-392 <MEN>
A;Cross-references: GB:M24406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-392 < KOI >
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A;Title: The poliovirus receptor protein is produced both
A;Reference number: S12048; MUID:91006015; PMID:2170108
A;Accession: A43024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C;Accession: A43024; B311496
C;Accession: A43024; B311496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 poliovirus receptor splice form delta precursor - N;Alternate names: poliovirus receptor H20B
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MPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTT
                                                                                                                                      FEKPOLLTVNĹTVYÝPÞEVSÍS-GYDNNWYLGQNEA-TLTCDARSNPEPTGYNWSTTMGP
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25.9%; Pred. No. 1.3e-09;
ative 54; Mismatches 176;
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	168 AMASKPATTIRWFKGNTELKGKSEVEEW-SDMYTVTSQLMLKVHKEDDGVPVICQVEHPA 226 168 STGGRPPAQITWHSDLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHES 227	유 성
	116ISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEV-NCT 167	g 4
E 41.	65 -QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS 115	B 8
	14 AAAAAAAPGLRLRLLLLEFSAAALIFTGDGQNLFTKDVTVIEGEVATISC- 64	9 8
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pro	Corper. Amer. Y: Politovilus receptor; minimungiopulin nomology Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane 1-20/Domain: signal sequence #status predicted <sig> 21-417/Product: poliovirus receptor alpha #status predicted <pvra> 21-343/Domain: extracellular #status predicted <ext> 21-343/Domain: extracellular #status predicted <ext></ext></ext></pvra></sig>	F;21
	graph pvs; pvs ss-references: GDB:120324; OMIM:173850 position: 19q13.2-19q13.2 position: 19q13.2-19q13.2 position: 19q13.2-19q13.2	A;Gene A;Cros A;Map A;Int
e H	9.00	A; Mol A; Res A; Cro C; Com
and e	55-865, 1989 ellular receptor for poliovirus: molecular cloning, nucleotide sequence, e number: A90910; MUID:89168426; PMID:2538245 n: A31496	Cell 5 A;Titl A;Refe A;Acce
	lso found rm has 331-Gly and lacks residues 332-384 Wimmer, E.; Racaniello, V.R.	A;NC R;NC
	,Accession: 512048 ;Molecule type: DNA ;Residues: 1-417 <roi> ;Cross-references: EMBL:X64116; NID:g35809; PIDN:CAA45478.1; PID:g825708</roi>	A; Mo A; Re A; Cr
ecreted	poliovirus receptor protein is produced both as membrane-bound and suber: S12048; MUID:91006015; PMID:2170108	A;Ti
Take	048; A31496 Tie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Take	R; Ko
	NSULT 12 HIUPA Liovirus receptor splice form alpha precursor - human Alternate names: poliovirus receptor H20A Contains: poliovirus receptor beta Species: Homo sapiens (man) Date: 30-Jun-1993 #sequence revision 30-Jun-1993 #text change 22-Jun-1999	RESULT RWHUPA poliov: N;Alte: N;Conta C;Spec: C;Date
	335SEHSGMSRNAIIFLVLGILVFLILLGIGIYF 365	Вb
	AVVVEAM	Ş
	286 LPPFAVAQGAQLLIRPVDKPINTTLICNVTNALGARQASLTVQVXEGPP 334	В

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neural cell adhesion molecule long domain form precursor - African clawed f. N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Datession: S09600
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A; Residues: 1-1088 <KRI>
A; Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610
A; Note: the authors translated the codon AAA for residue 970 as Leu
C; Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
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Nucleic Acids Res. 17, 10321-10335, 1989
A.Title: Primary structure and developmental expression
A.Reference number: S09600; MUID:90098871; PMID:2481269
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7,129-188/Domain: immunoglobulin homology <INM2>
7,149-153/Region: heparin binding #status predicted
7,158-162/Region: heparin binding #status predicted
7,225-284/Domain: immunoglobulin homology <INM3>
7,317-381/Domain: immunoglobulin homology <INM3>
7,413-475/Domain: immunoglobulin homology <INM4>
7,413-475/Domain: immunoglobulin homology <INM5>
7,512-589/Domain: fibronectin type III repeat homology <FN3A>
7,518-679/Domain: fibronectin type III repeat homology <FN3B>
7,706-723/Domain: transmembrane #status predicted <INM>
7,706-723/Domain: intracellular #status predicted <INT>
7,741-088/Domain: intracellular #status predicted <INT>
7,741-088/Domain: intracellular #status predicted <INT>
7,41-108/Jomain: intracellular #status predicted <INT>
7,41-3,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
7,41-3,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
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20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <9.07-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status j.20-705/Domain: extracellular #status predicted <EXT>
34-95/Domain: immunoglobulin homology <IMM1>
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89; Conserva
DDGVPVICQUEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGK 272
                                                                                                                                                                           EBIEVNCTAMASKPATTIRW-----FKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKE 212
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                                                                                                         DEITLTCEA-SGDPIPSITWRTAVRNISSEATTLDGHIVVKEHIRM----SALTLKDIQY
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neurotrimin - rat
(C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Accession: I56551
C;Accession: I56551
J. Neurosci. 15, 2141-2156, 1995
A;Title: Cloning of neurotrimin defines a new subfamily of differentially expressed
A;Reference number: I56551; MUID:95198094; PMID:7891157
A;Accession: I56551
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C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42633
R;Yajima, H; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.;
Biochem. Biophys. Res. Commun. 223, 160-164, 1996
A;Title: A 11.5-kb 5'-terminal 203, 160-164, 1996
A;Title: A 11.5-kb 5'-terminal 203, 160-164, 1996
A;Reference number: Z22221; MUID:96254045; PMID:8660363
A;Accession: T42633
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c;Species: Gallus gallus (chicken)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C;Accession: T42633
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,Residues: 1-4162 </AJ>
,Cross-references: EMBL:D83390; NID:g1513029; PIDN:BAA11908.1;
,Experimental source: breast muscle
;Keywords: skeletal muscle
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       Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TDHKY-KISFFNKVSGLKILNAGLEDSGEYTFEVKNSVGKSSCTASLQVSDRIMPPSFTR 3657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISVLWLKDKGEII------RESENLWISYSENVASLKIGNAEPTNAGKYICQIKNDAG 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVIQLINDURQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPP 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKVNGLQESDMGTYSCTATNVAGSDECSAFLSVREPPSFVKKPEPFNVLSGENITFTSIV 3769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QESYTTITYLVPPRNLMIDIQXDTAVE---GEEIEVNCTAMASKPATTIRWFKGNTELK 187
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EMBL:U16845; NID:g755184; PIDN:AAA67445.1; PID:g755185
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Pred. No. 1.3e-07;
O; Mismatches 155;
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Best Local
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                                                                                                                                                                                                                   SQLMLKVH---KEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGL-TR 258
                                                                                                                                                                                                                                                                                      PRNIMIDIQKDTAV-EGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVT
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                                                NYTCVASNKLGHTNASIMLF
                                                                                  TYRCEASNIVGKAHSDYMLY 329
                                                                                                                 VGQKGTLQCEASAVPS-AEFQWFKDDKRLVEGKKGVKVENRPFLSRLTFP--NVSEHDYG 291
                                                                                                                                                                                   REQSGEYECSASNDVAAPVVRRVN------VTVNYPPYIS-----EAKGTGVP 234
                                                                                                                                                                                                                                                      PK--IVEISSDISINEGNNISLTCIA-TGRPEPTVTWRHISPKAVGFVSEDBYLEIQGIT
                                                                                                                                                 EGDALELTCEAIGKPQPVMVTWVRVDDEMPQ-----HAVLSGPNLFINNLNKTDNG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%; Score 230; DB 2; 26.2%; Pred. No. 5.6e-09;
2004, 06:00:27
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Search completed: July Job time: 34.7249 sec: 7,

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Result
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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P13591 homo sapien	Q08180 drosophila		046631 bos taurus				060500 homo sapien	Q62813 rattus norv			

ALIGNMENTS

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MBL; AF308632; AAG30281.1; SSP, P06907; INEU. INEUTPO; IPRO07110; Ig-like. InterPro; IPRO0710; Ig-like. IPRO0740; ig; 2. MART; SM00406; IGv; 1. MART; MR00406; IGv; 1. MART; MR00406; IGv; 1. MART; MR00406; IGv; 1. MART; SM00406; IGv; 1. MART; SM00406	Cohen G.H.; ("Porcine HyeC, a member of the highly conserved HyeC/nectin 1 family, is a functional alphaherpesvirus receptor.") ("Porcine HyeC, a member of the highly conserved HyeC/nectin 1 family, is a functional alphaherpesvirus receptor.") ("Porcine HyeC, a member of the highly conserved HyeC/nectin 1 family, is a functional alphaherpesvirus receptor.") ("Porcine HyeC, and hy	ı,t

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Matches 108
                        SEQUENCE FROM N.A. (ISOF MEDILINE=95237621; PubMed Lopez M., Eberle F., Mat Dubreuil P.; "cDNA characterization a
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Poliovirus receptor related protein 1 precursor (Hemediator C) (HyeC) (Nectin 1) (Herpesvirus Ig-like
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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F., Mattei M.-G.,
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                                                                               Gabert
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Nat. Genet. 25:427-430(2000).
Nat. Genet. 25:427-430(1000).
-1- FUNCTION: PROBABLY INVOLVED IN
-1- FUNCTION: PROBABLY (HSV-1, HSV-2)
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restrue by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lopez M., Cocchi F., Avitabile E., Lec Campadelli-Fjume G., Dubreuil P.; "Novel, Boluble isoform of the herpes nectin1 (or prr1-HIGR-Hvec) modulates susceptibility to hsv infection."; J. Virol. 75:5684-5691(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM GAMMA).
MEDLINE=21256041; PubMed=11356977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Entry of alphaherpesviruses mediated protein 1 and policvirus receptor."; Science 280:1618-1620(1998).
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Spear P.G.;
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                                                                                                                                                                                                                                                                                                                    IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
DISBASE: Defects in PVRII are a cause of cleft lip/palate-
ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1 is 
responsible for allelic forms known as Margarita island ectodermal 
dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
DATABASE: NAME=PROW 2:45-49(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I memb delta). Secreted (isoform gamma). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Interacts with HSV glycoprotein D SUBCELLULAR LOCATION: Type I membrane prote
                                                                                                                                                                                                                                                                                                           WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Gamma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Delta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative
          AF252867,
AF196769,
AF196770,
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AF196771,
AF196774,
AF196778,
AF196769,
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AY029539;
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AAG166440.
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                                                                                                                                                   AAK33124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence=VSP_002626,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        splicing; Named isoforms=3;
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AND PSEUDORABIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       poliovirus receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Α.,
                                                                                                                                                                                                                   . Usage by and for http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                       VSP_002627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richieri-Costa
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Matches 105
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MIM; 600644;
MIM; 225060;
MIM; 225060;
GO; GO:001602
GO; GO:000459
GO; GO:000595
InterPro; IPR
                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
CARBOHYD
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DISULFID
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CARBOHYD
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
Cell adhesion; Immunoglobulin
                                                                                                                                                                                                                                                                           VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0016021;
GO:0004895;
GO:0015026;
GO:0006955;
244
                                   191
                                                     188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR007110; Ig-like.
IPR003596; Ig_v.
                                                                                       QESYTTITYLVPPRNLMIDIQXD-TAVEGEEIEV---NCTAMASKPATTIRWFKGNTELK 187
                                                                                                         IQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPP--
QYEPEVTIEGFDGNWYLQRMD----
                                                    GKSEVEEW---
                                                                      RESQLNLTVMAKPTNWIEGTQAVLRAKKGQDDKVLVATČTSANGKPPSVVSW----ETRLK
                                   GEAEYQEIRNPNGTVTVISRYRLVPSREAHQQSLACIV-
                                                                                                                                                                                   517
                                                                                                                                                                                                                                                                                                                          353
                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:integral to membrane; NAS F:cell adhesion receptor ac F:coreceptor activity; TAS P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                          517
                                                                                                                                                                                                                                                                            458
                                                  -SDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRY-----LEV
                                                                                                                                                                                   57158
                  -MTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGP
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25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal;
                                                                                                                                                       5.2%
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                                                                                                                                                60;
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.

CYTOPLASNIC (POTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

POLY-GLU.
                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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SPEYTPSPPEHGRRAGPV -> 1
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BY SIMILL
BY SIMILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain; Receptor; Transmembrane; Alternative splicing. POTENTIAL. POLIOVIRUS RECEPTOR RELATED PROTE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                    /FTId=VSP 002625;

FPYTPSSPEHGRAGEVPTAIIGGVAGSILLVLIVVGGIVV
ALARRHTFRGDYSTKAGDYSTKAGTPGHEPVAQNLQ
YPDDSDDEKKAGPLGGSSYEEBEBEBEGGGGERKVGGPHP
- KRRPORGLGSARKLLAGTVAVFLILVAVLTVFFLYNRQ
OKSPPETDGAGTDQPLSQKPEPSPSRQSSLVEBIQVVHLD
PGRQQQDEBEDLQKLSLQPYYDLGVSPSYHPSVRTTEPRG
ECP_iin_isoform_Alpha).
                                                                                                                                               Score 256.5; DB 1
Pred. No. 4.7e-11;
D; Mismatches 154
                                                                                                                                                                                  Missing (In isoform Alpha).
/FTId=VSP_002627.
DF34CBAEC893EE6D CRC64;
                                                                                                                                                                                                                                                                                              (in isoform Gamma).
/FTId=VSP 002624.
Missing (In isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane; NAS.
                                                                                                                                                                                                              /FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY.
SIMILARITY.
SIMILARITY.
--VKLTCKADANPPATEYHWTTLNGSLPKGVEAQNR
                                                                                                                                                                                                              002626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity; NAS
                                                                                                                                                               DB 1;
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                                                                                                                                                                Length
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(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
                                     NYHMDREKESLTLNV
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PVR2 MOUSE STANDARD; PRT; 530 AA.

ID PVR2 MOUSE STANDARD; PRT; 530 AA.

AC P32507; Q62096;
DT 01-CCT-1993 (Rel. 27, Created)
DT 16-CCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Muserland OR PVR OR NPH.

OS Mus musculus (Mouse).
   TARRER REPRESE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ś
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                                                                                                                                                                                                             RX MEDILINE-2238857; Pubmed-12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Cellins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Balakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Balakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

RT human and mouse cDNA sequences.",

Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CHARACTERIZATION.

MEDLINE=99214397; PubMed=10196354;
Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
"The murine homolog (Mph) of human herpesvirus entry protein
mediates entry of pseudorables virus but not herpes simplex v
types 1 and 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A., "Amino acid residues on human poliovirus receptor invo interaction with poliovirus.", J. Biol. Chem. 269:8431-8438(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and expression poliovirus receptor gene.";
J. Virol. 66:2807-2813(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFOR MEDLINE=92219365; PubMed=1 Morrison M.E., Racaniello
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM BETA).
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=94179228; PubMed=8132569;
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6; TISSUE=Brain;
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INTO CELLS.
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CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                                                                                VARSPLIC
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SMART; SM00405; IGv; II
PROSITE, PS50855; IG LIKE; 3.
Immunoglobulin domain; Recept
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A38211; HLMSP3.
A53437; A53437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:97822; Pvrl2
    57
                                          67
                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M80206; AAA39734.1; -. D26107; BAA05103.1; -. BC059941; AAH59941.1; -.
                                                                              N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P32507-2; Sequence=VSP_002630, VSSUE SPECIFICITY: Brain, spinal cord,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P32507-1; Sequence=Displayed
                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative
  LPPTTERVSQVTWQRLDGTVVAAFHPS
                                                                            ARAAVLPPSRLSPTLPLLPLLLL----LLQETGAQDVRVRVLPEVRGRLGGTVELPCHL
                                                                                                                  AAAAAAPPG-----LRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEV---ATISCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73:4493-4497(1999).
CON: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY
                                                                                                                                                                                                                                          530 AA;
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contains
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351
372
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                                                                                                                                                                                                                                          57317
                                                                                                                                                                             10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          splicing.
                                   -NKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQL------LNFSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

SPSTMAGAGTGGIIGALIAAIIATAVAGTGILICROORKE

ORLOAADEEEEBLEGPPSYKPFTPAKLEEPENESQLFTLAG

SEHSPVETPYPDAGUSCANDOMNERYHELPTLEERSGPLLGA
SEHSPVETPYPDAGUSCANDOMNERYHELPTLEERSGPLLGA
ATGLGP -> DTPQASRDVGPLVWGAVGGTLLVLLLAGGFL

ALILLRORRERESGEGGGONDGDRGSYDFTOVFGNGGPVFW

BYANSPENDER DDCREETER NA DENEE SYDNAM

BYANSPENDER DCREETER DENEE DENEE DENEE DENEE D
                                                                                                                                                        63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin-like V-type domain. immunoglobulin-like C2-type domains.
                                                                                                                                                                           Score 247.5; DB 1
Pred. No. 2.2e-10;
                                                                                                                                                                                                                                                           Missing (in isoform Alpha).
/FTId=VSP_002631.
                                                                                                                                                                                                                                                                                                                  ESHLDGSLISRRAVYV (in isoform
                                                                                                                                                                                                                                                                                                                                       RSASPEPMRPDGREEDEEEEEEMKAEEGLMLPPHESPKDDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLICVIRUS RECEPTOR RELATED EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                 FTId=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                        0ED71BFA2B231BBE CRC64;
                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                 002630.
-FGVDFPNSQFSKDRLSFVRARPETNADLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
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, spleen, ki
                                                                                                                                                          166;
                                                                                                                                                                                            Length
                                                                                                                                                          Indels
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                                                                                                                                                        91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heart
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112
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RESULT 4
PVR_CERAE
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EMBL; D12611; BAA02136.1; -. EMBL; D12612; BAA02137.1; -. PIR; A44194; A44194.
                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVR_CERAE
P32506;
                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Type
Secreted (isoforms beta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kolke S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.; "A second gene for the African green monkey poliovirus receptor that has no putative N-glycosylation site in the functional N-terminal immunoglobulin-like domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Poliovirus receptor precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93059651; PubMed=1331508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVR OR PVS.
                                                                                                                                                                                        SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                        Name=Gamma
                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Not known. Used by poliovirus to bind and enter the
                                                                                                                                                                                                                                                                                                                                        Name=Alpha;
                                                                                                                                                                                                                                                                                                                                                     Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342
                                                                                                                                                                                   IsoId=P32506-2; Sequence=VSP_002622, VSP_002623;
IMILARITY: Contains 1 immunoglobulin-like V-type domain.
IMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335
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                                                                                                                                                                                                                                                       IsoId=P32506-4;
                                                                                                                                                                                                                                                                                     IsoId=P32506-3;
                                                                                                                                                                                                                                                                                                                  IsoId=P32506-1; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A. (ISOFORMS ALPHA AND DELTA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V------NCTAMASKPATTIRWFKG-NTELKGKSEVEEWSDMYTVTSQLMLKVHKEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPEN---
                                                                                                                                                                                                                                                                                                                                                                                                                                               66:7059-7066(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTDYDWSTTSGVFPASAVAQGSQLLVHSVDRMVNTTFICTATNAVGTGRAEQVILVRESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cercopithecus.
                                                                                                                                                                                                                                                     Sequence=Not described;
                                                                                                                                                                                                                                                                                     Sequence=Not
                                                                                                                                                                                                                                                                                                                                                  splicing; Named
                                                                                                                                                                                                                                                                                                                                                                                  and gamma).
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                                                                          noved. Usage by and fo
(See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                    isoforms=4;
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DOMAIN
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TRANSMEM
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PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; SMART; SM00406; IG
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                 Local
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                404
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370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative
                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                  SDDSVIQLLNPNR-----QTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS-----I
                                                                                                                                                                                                                                                    ARTMAAAWPP-----LLLTLLELSWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPG
                                                                                     QHAVLSGENLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTT
                                                                                                                 GNLQTQRYLEVQYXPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMP
                                                                                                                                          PPAHITW---HSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTCKVEHESFE
                                                                                                                                                                              EDEGNYTC
                                                                                                                                                                                               SDEGRYFCQLYTDPPQESYTT---ITVLVPPRNLMIDIQKDTAVEGEEIEV-NCTAMASK
                                                                                                                                                                                                                MEETHVSQLTWSRHGESGSMAVFHQTQGPNYSEPKRLEFVAARLGTELRDASLRMFGLRV
                                                                                                                                                                                                                                                                      AAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTV--IEGEVATISC--QVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR007110;
IPR003596;
CSREFLWCHHLSPSSEEHASA--
                GT---
                                                   TTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIIL----
                                                                     PFAVAQGAQLLIRPVDKPINTTFICNVTNALGARQAELTVQVKEGPPSEPSGMSSN----
                                                                                                        KPQLLTVNLTVYYPPEVSIS-GYDNNWYLSQNEA-TLTCDARSNPEPTGYNWSTTMGPLP
                                                                                                                                                            PATTIRWFKGNTELKGKSEVEE----WSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVT
                                                                                                                                                                                                                                                                                                                           417
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                             -YFTHEAKGADDAADADTAIINAEGGONNSEEKKE
                                                                                                                                                                                                                                                                                                                           ₽,
                                                                                                                                                                              LFVTFPQGSRSVDIWLRVLAKPQN-TAEVQK-VQLTGKPVPVARCVSTGGR
                                                                                                                                                                                                                                                                                                                                                             splicing
20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig-like.
Ig_v.
                                                                                                                                                                                                                                                                                                                           45464
                                                                                                                                                                                                                                                                                               10.7%;
                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                       70;
                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POT IG-LIKE V-TYPE. IG-LIKE C2-TYPE IG-LIKE C2-TYPE BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. N-LINKED (GLCNAC)
                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                               Score 244;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                         EHASASA -> HHQSCHN (in isofe

/FTIG-VSP 002622.

Missing (In isoform Delta).

/FTIG-VSP 002623.

; DA4ADDFE4D276E1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLIOVIRUS REC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                        Mismatches
-SANGYISYSDVSRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                       192;
                                  IIIFLILGIVÍLLTLLGIGVÝFYRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
                                                                                                                                                                                                                                                                                                         Length
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(POTENTIAL).
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                                                    GRYFARHK
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RESULT 5
PVR2_HUMAN S
ID _PVR2_HUMAN S
AC Q92692; O75455;

STANDARD; Q96J29;

PRT;

538

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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K.J., Farmer A.A., Rubin G.M., Hong L.,
RA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Rahes J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J. W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse CDNA sequences.",
[A] Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I., Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G., "A cell surface protein with herpesvirus entry activity (HveB) susceptibility to infection by mutants of herpes simplex virus type 2, and pseudorables virus.", Virology 246:179-189(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Poliovirus receptor related protein 2
mediator B) (HyeB) (Nectin 2) (CD112 a
PVRL2 OR PRR2 OR HYEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM Aurting), SEQUENCE 98321161; PubMed=9657005; MEDLINE=98321161; Partinez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLLINE=95347610; PubMed=7622062;
Eberle F., Dubreuil P., Mattei M.-G., Devilard E., Lop
"The human PRR2 gene, related to the human politovirus
(PVR), is the true homolog of the murine MPH gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM ALPHA). TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 159:267-272(1995).
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                                                                                                                                          -i-
                                                                                                                                                                                            SEQUENCE OF 449-538 FROM N.A.

MEDLINE-99449047; PubMed=10520737;

Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K.,

Ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.;

"Sequencing of 42kb of the APO 3-C2 gene cluster 1
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257;
                                                                                                                                                                           "Sequencing PEREC1.";
                                                                                                                                                                                                                                                                                                                        sequencing
                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 31-538 FROM N.A. Yoshiura K. Murray J.C., Washiura K. Murray J.C., The Transcriptional map in the
                                                               NA Seq. 9:89-101(1998).

PUNCTION: RECEPTOR FOR ALPHA
PESUDORABIES VIRUS) ENTRY IN
SUBCELLULAR LOCATION: Type I
ALTERNATIVE PRODUCTS:
EVent=Alternative splicing;
                                                    Name=Delta;
IsoId=Q92692-2;
                                  IsoId=Q92692-1;
                                                                                                                                                                                                                                                                                                        (JAN-1998) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=12477932
                                                                                                                                                                                                                                                                                                        trapping.
Sequence=VSP_002628,
                                Sequence=Displayed
                                                                   splicing;
                                                                                                                           FOR ALPHAHERPESVIRUS ) ENTRY INTO CELLS.
                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                           region
                                                                       Named
                                                                                                          membrane
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2 precursor
2 antigen).
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irus receptor
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Mullahy S.J.,
naratne P.H.,
J., Hulyk S.W.,
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Best Local S
Matches 111
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GO; GO:0005886; C:plasma membrane; TAS.

GO; GO:0015026; F:coreceptor activity; TAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003599; Ig.

Pfam; PF00047; Ig; 1.

SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.
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EMBL; AF04496
EMBL; AF04496
EMBL; AF05015
PIR; 168093;
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modified and this statement is not removed.
entitles requires a license agreement (See r
or send an email to license@isb-sib.ch).
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Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: Ubiquitous.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 immunoglobulin-like C-type domain.
DATABASE: NAME=PROW; NOTE=PROW 174-77 (2000);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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AF050154; AAD02503
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                                                                                                          N
                                                                                                                                                                                                                                                     Similarity
VELPCHLLPPVPGLYISLVTWQRPDAPANHQNV--AAFHPKMGPSFPSPKPGSERLSFVS
                                                                                                             ARAAALLPSRSPPTPLLWPLLLLL----LLETG-AQDVRVQVLPEVRG
                                                                                                                                                         SQCAAAAAAAAPPGLRLRLLLLLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKS
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POTIOVITAL (POTENTIAL).

POTENTIAL (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE 1.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

SPLENDEDLEGPPSYKPETPKAKLEAQEMPSQLFTLGASEH
SPLENTYPEDAGASCTEGEMPKYHELFFLEERSGPLH-GGATS

SPLENTYPEDAGASCTEGEMPKYHELFTLINGTY

SPLENTYPEDAGASCTEGEMPKYHELFTLINGT
                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                    Score 242.5;
Pred. No. 5e-1
66; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGSPIP -> RASPRDVGPLVWGAVGGTLLVLLLLAGGSLA
FILLRVRRRRKSPGGAGGGASGDGGFYDPKAQVLGNGDPVF
WTPVVVGGPMEPDGKDEEEEEEEEKAEKGLMLPPPPALEDDM
                                                                                                                                                                                                                                                                                                                                                         Missing (In isoform Alpha).
/FTId=VSP_002629
                                                                                                                                                                                                                                                                                                                                                                                                                    ESQLDGSLISRRAVYV (in isoform /FTId=VSP_002628.
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No. 5e-10;
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                                                  "Sequence analysis of a IMb region in 19q13.2 gene cluster.";
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=89168426; PubMed=2538245;

Mendelsohn C.L., Wimmer E., Racaniello V.R.;

Mendelsohn C.L., Wimmer E., Racaniello V.R.;

"Cellular receptor for poliovirus: molecular cloning, nucleotide
"Cellular receptor for poliovirus: molecular cloning, nucleotide
sequence, and expression of a new member of the immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                        Poliovirus receptor precursor (CD155 antigen)
MEDLINE=91239515;
Koike S., Ise I.,
                                                                                                                                                             Koike S., Horie H., Ise I., Okits Takeuchi K., Takegami T., Nomoto
                                                                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE MEDLINE=91006015; PubMed=2170108;
                                                                                                                                                                                                                      Racaniello V.R.;
Submitted (JUL-1995)
                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                       DOMAINS
                                               Submitted
                                                                                                                                        "The poliovirus receptor protein and secreted forms.";
                                                                                                                                                                                                                                             REVISIONS.
                                                                                                                                                                                                                                                                                 superfamily."
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                            J. 9:3217-3224(1990).
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                                             (MAY-2000)
PubMed=1851992, Nomoto A.;
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                                            to the
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                                            EMBL/GenBank/DDBJ
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function of the human poliovirus receptor."
J. Virol. 66:7368-7373(1992).
-!- FUNCTION: Not known. Used by poliovirus
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"N glyc
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the European Bioinformatics Institute. The
use by non-profit institutions as modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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Zibert A., Wimmer
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Proc. Natl.
  888888
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bert A., Wimmer E.;
glycosylation of the virus binding domain
nction of the human policvirus receptor.";
Virol. 66:7368-7373(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 2 immunoglobulin-like C2-type domain DATABASE: NAMES-PROW; NOTE=CD guide CD155 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd155.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND VIRUS BINDING AND UPTAKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type delta). Secreted (isoforms
; 173850; -.
GO:0005737; C:cytoplasm; TAS.
GO:0005615; C:extracellular space; TA
GO:0016021; C:integral to membrane; T
GO:0004872; F:receptor activity; TAS.
GO:0004872; F:invasive growth; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Delta;
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Event=Alternative splicing; Named isoforms=4;
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M24406; AAA36462.1;
X64116; CAA45478.1;
X64117; CAA45478.1;
X64118; CAA45478.1;
X641120; CAA45478.1;
X64121; CAA45478.1;
X64122; CAA45478.1;
X64123; CAA45479.1;
X64123; CAA45479.1;
X64116; CAA45479.1;
X64117; CAA45479.1;
X64118; CAA45479.1;
X64118; CAA45479.1;
X64119; CAA45479.1;
X64112; CAA45479.1;
X64122; CAA45479.1;
X64123; CAA45480.1;
X64113; CAA45480.1;
X64112; CAA45480.1;
X64112; CAA45480.1;
X64112; CAA45480.1;
X64122; CAA45480.1;
X64122; CAA45480.1;
X64122; CAA45480.1;
X64123; CAA45480.1;
X6412
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                                                                                              A43024;
S12048;
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                                                                                 143024; RWHUPD.
312048; RWHUPA.
HGNC:9705; PVR
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SMART; SM00406; IG
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InterPro; IPR003596;
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                                                                                                                                                                                                                                                                                   LQVPNMEVTHVSQLTWARHGESGSMAVFHQTQGPSYSESKRLEFVAARLGAELRNASLRM
                                                           LPPFAVAQGAQLLIRPVDKPINTTLICNVTNALGARQAELTVQVKEGPPS
                                                                                                                FEKPOLLTVNTLTVYYPPEVSIS-GYDNWYLGQNEA-TLTCDARSNPEPTGYNWSTTMGP
                                                                                                                                         VTGNLQTQRYLEYQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDE
                                                                                                                                                                        STGGRPPAQITMHSDLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHES
                                                                                                                                                                                                   AMASKPATTIRWFKGNTELKGKSEVEEW-SDMYTVTSQLMLKVHKEDDGVPVICQVEHPA
                                                                                                                                                                                                                              FGLRVEDEGNYTC-LEVTFPQGSRSVDIWLRVLAKPQN-TAEVQK-VQLTGEPVPMARCV
                                                                                                                                                                                                                                                     ---ISDEGRYFCQLYTDPPQESYTT---ITVLVPPRNLMIDIQKDTAVEGEBIEV-NCT
                                TTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYF
                                                                                       MPQHAVLSGPNLFINNLNKTDNGTYRCEASNI VGKAHSDYMLYVYDPPTTI PPPTTTTTT
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226 167 167 110

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PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Receptor;
Repeat; Antigen; Alternative sp.:
                   AAAAAAAPPGLRLRLLLLLESAAALIPTGDGQNLFTKDVTV-----IEGEVATISCQ
ARAMAAAWPILLVALLVISWP-----PPGTG-----DVVVQAPTQVPGFLGDSVTLPCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig-like.
Ig_v.
                                                    10.5%;
                                                                                      WW,
                                            53
                                           Score 240; DB
Pred. No. 5.5e-
53; Mismatches
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N-LINKED
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IG-LIKE
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I -> M (in dbSNP:203710).
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(in isoform
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Beta).
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                                            76;
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                                             Gaps
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                        65
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GO; GG:0005913; C:cell-cell adherens ju
GO; GG:0005915; F:protein binding; IPI.
GO; GG:0004872; F:receptor activity; ID
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 2.
Cell adhesion; Immunoglobulin domain; F
Repeat; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVR1 MOUSE STANDARD; PRT; 515 AA.

Q9VKF6; Q9SEL5; Q9JI17;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Poliovirus receptor related protein 1 precurse

mediator C) (HveC) (Nectin 1).

PVRL1 OR PRR1 OR HVEC.

Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repeat; Glycoprotein; SIGNAL 1 . 3
                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                               entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-2000) to the EMBI/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          floor plate during embryogenesis, suggesting a role development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDILINE=20541977; PubMed=11090177;

MEDILINE=20541977; PubMed=11090177;

Shukla D. Dal Canto M.C., Rowe C.L., Spear P.G.;

"Striking similarity of murine nectin-lalpha to human nectin-lalpha (HveC) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry."

alphaherpesvirus entry."

J. Virol. 74:11773-11781(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20243787; PubMed=10781093;
Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi
Lecocq E., Dubreuil P., Campadelli-Fiume G.;
"The murine homolog of human nectin1 delta serves as
"Onspecific mediator for entry of human and animal al
in a pathway independent of detectable binding to gD.
proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Swiss Webster; Zhan J., Wimmer E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                               send
                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Interacts with HSV glycoprotein D (gD).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 1 immunoglobulin-like V-type d
SIMILARITY: Contains 2 immunoglobulin-like C2-type
                                                                                                                                                                                  ; AF239762; AAF60333.1; -.; AF270977; AAF76195.1; -.; AF297665; AAG22808.1; -.; MGI:1926483; Pvrll.
                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                               requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
· 30
POTENTIAL. POLIOVIRUS
                                            domain; Receptor;
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                                                                                                                          .; IPI.
.; IDA.
                                                                                                                                                                     junction; IDA
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RECEPTOR
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; Murinae; Mus
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Best Local S
Matches 98
Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                  -NCA1 XENLA
P16170;
01-APR-1990
01-APR-1990
15-MAR-2004
Neural cell
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adhesion molecule 1, 180 k
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CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
POLY-GLU.
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Pred. No. 8.5e-10
9; Mismatches 14
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Gaps

SALTLKDI

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InterPro; IPR008957; FN_III-like.
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003598; Ig_cl2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR00041; fn3; 2.
InterPro; IPR00041; In3; 2.
InterPro; IPR00040; IN3; 2.
INTERPRO0040; IN3; 2.
INTERPRO00408; IGC2; 5.
INTERPRO004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S09600; IJX
HSSP; P56276; 1T
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SIMILARITY: Contains 5 immunoglobulin-like C2-type d
SIMILARITY: Contains 2 fibronectin type III domains.
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Name=N-CAM 140;
IsoId=P16170-2; Sequence=VSP 002589
TISSUE SPECIFICITY: Expressed In neur
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SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
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FUNCTION: This protein is a cell adhesion
neuron-neuron adhesion, neurite fascicula
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Hahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Hakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
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STRAIN=ICR; TIS
Kim T.H., Choi
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Kim T.H., Choi S.C., Kim J.
"Cloning and expression of
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SMART; SM00409; IG; 3.
SMART; SM00408; IGC2; 3.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG LIKE; 3.
Immunoglobulin domain; Cell a
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InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig_c2.
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                                                                                                                                                                                       SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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FUNCTION: Neural cell adhesion molecule.
SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
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SQLMLKVH---KEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGL-TR
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MEDLINE=95198094; PubM
Struyk A.F., Canoll P.I
Salzer J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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01-NOV-1997 (Rel. 35, Last se
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Neurotrimin precursor (GP65).
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SMART; SM00408; IGc2; 2.
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28-FEB-2003
10-CCT-2003
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Li G., Jin J., Than X., Hu S., Yuan J., Qiang B.;
Li G., Jin J., Than X., Hu S., Yuan J., Qiang B.;
"Cloning and identification of human neurotrimin full le
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Neural cell adhesion molecule.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a
-!- SIMILARITY: Belongs to the immunoglobulin superfamil
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Q9P121;
        EMBL; AF126426; AAF37591
MIM; 607938; -.
GO; GO:0008038; P:neuron
                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria; Primates;
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Pred. No. 2.2e
53; Mismatches
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RESULT 12

NCM2 MOUSE

ID NCM2 MOUSE

AC 03513; 035962;
DT 15-UUL-1998 (Rel. 36, Created)
DT 15-UUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2)
DE adhesion molecule) (ReH12).
GN Mus muscults (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
NCHI TaxID=10090;
RN CSTRAIN=BALB/C; TISSUB=Olfactory neuroepithelium;
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Immunoglobulin domain; Cell a
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rPro; IPR003598;
; PF00047; ig; 3.
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                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                 YFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTD-PPQESYTTITVLVP
                                                                                                                                                                                          LRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAMLNRSTIL
TCVASNKLGHTNASIMLF
                 RCEASNIVGKAHSDYMLY
                                               EGDALELTCEAIGKPQFVMVTWVRVDDEMPQH----AVLSGP---NLFINNLNKTDNGTY
                                                                                     PRNLMIDIQKDTAV-EGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVT
                                   VGQKGTLQCEASAVPS-AEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNY
                                                                          REQSGDYECSASNDVAAPVVRRVK--
                                                                                                               PK--IVEISSDISINEGNNISLTCIA-TGRPEPTVTWRHISPKAVGFVSEDEYLEIQGIT
                                                                                                                                                     YAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHLIVQVS
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Ig_c2.
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Pred. No. 3.1e.
54; Mismatches
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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Craniata; Vertebrata; Sciurognathi; Muridae;

Euteleostomi; ; Murinae; Mus

2)

(RB 8

neural

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or send a
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                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alenius M., Bohm S.;
"Identification of a novel neural cell adhesion molecule-related with a potential role in selective axonal projection.";
J. Biol. Chem. 272:26083-26086(1997).
                                                                                                                                                                                                                                                                     Pfam; PF00041; fn3; 2
Pfam; PF00047; ig; 5.
                                                                                                                                                                                                                                                                                                                                    EMBL; AF001287; AABS9125.1; -.
EMBL; AF001286; AABS9124.1; -.
EMBL; AF016619; AACS3375.1; -.
MGD; MGI:97282; NCam2.
                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long a modified and this statement is not removed.
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STRAIN=C57BL/6J; TISSUE=Olfactory (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97368238; PubMed=9221781;
Yoshihara Y., Kawasaki M., Tamada A., Fujita H.,
Kagamiyama H., Mori K.;
"OCAM: A new member of the neural cell adhesion
                                                                                                                                                               DOMAIN
                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                       InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97476194;
                                                                                                                                                                                                                 mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                         cities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurosci. 17:5830-5842(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: May play important roles in selective fasc zone-to-zone projection of the primary olfactory axc SUBCELLULAR LOCATION: Type I membrane protein (long attached to the membrane by a GPI-anchor (short isof ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=O35136-2; Sequence=VSP_002590; TISSUE SPECIFICITY: Expressed in subsets of both olfactory vomeronasal neurons in a zone-specific manner. SIMILARITY: Contains 5 immunoglobulin-like C2-type domains SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a cyeen the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=035136-1; Sequence=Displayed;
                                                                                                                                                                                                                                     SM00060; FN3; 2.
SM00408; IGC2; 5.
E; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to zone-to-zone projection
Transmembrane; Glycoprotein; Repeat; domain; Signal; GPI-anchor; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                         AAB69125.1; -.
AAB69124.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=9334170;
 υ
                                                                                 POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.
PROBABLE.
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                                                                                                                                                                                              CELL ADHESION MOLECULE
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(GLCNAC.
(GLCNAC.
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RESULT 13

NCA2 ENLA

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Best Local
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NCA2_XENLA

P36335;

01-JUN-1994

01-JUN-1994

15-MAR-2004

Neural cell
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CARBOHYD
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VARSPLIC
                                                                                                                                                                        Tonissen K.F., Krieg P.A.;
"Two neural-cell adhesion molecule (NCAM)-encoding genes in Xen
"Two neural-cell adhesion development and in adult tissues.";
laevis are expressed during development and in adult tissues.";
Gene 127:243-247(1993).
-!- FUNCTION: This protein is a cell adhesion molecule involved
                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Ven
Amphibia, Batrachia, Anura, Mesobatrachia,
Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neural
                                                                                                                                                                                                                                                                                    MEDLINE=93273239; PubMed=7684721;
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCAM2.
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                                                                                     neurites, etc.
SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
                                           Event=Alternative splicing; Named Comment=A number of isoforms are
                                                                                                                                                                                                                                                                                                                                                  _TaxID=8355;
                                                                                                                                                       neuron-neuron adhesion,
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  IsoId=P36335-1; Sequence=Displayed
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Best Local 9
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InterPro; IPR008957; FW III.
InterPro; IPR003961; FW III.
InterPro; IPR003598; Ig_like.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn3; 2.
Pfam; PF00047; ig; 5.
SMART; SM00408; IG_2; 4.
SMART; SM00408; IG_2; 4.
SMART; SM00408; IG_2; 4.
SMART; SM00408; IG_1KE; 5.
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PROSITE; PS50835; IG_LIKE; 5.
Cell adhesion; Glycoprotein; Transmembrane; Repeat; Cell adhesion; Glycoprotein; Transmembrane; Repeat; Cell adhesion; Glycoprotein; Alternative splicing; Signal.

Immunoglobulin 19 By SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (So or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lified and this statement is not removed. Usage by and for commercial integratives alicense agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY:
SIMILARITY:
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373
                   214
                                         317
                                                              160
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                                                                                                      100
                                                                                                                             199
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                                                                                                                                                50
                                                                                                                                                                                Similarity
                                                                                  ISFNEDKSEMTIYRVEKEDEAEYSC-IANNQAGEAEAIVLLKVYAKPKWTYVENKTTVEL
                                                                                                      LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG
                                                                                                                                              KDVTVIEGEVATISC----QVNKS----DSVIQLLN----PNRQTIYFRDFRPLKDSRFQL
DAGEYFCVASNP-IGVDMQAM-YFEVQYAPKIR----GPVVVYTWEGNPVNITCDVLAHP
                   DGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKP
                                                              EEIEVNCTAMASKPATTIRWFKGNTELKGKSEVBEWSDMYTVT-----
                                                                                                                            KDIQVIVNVPPLIQARQIRVNATANMDESVVLSCDADGFPDPEISWLKKGEPIEDGE-EK
                                                                                                                                                                                                                1092
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Contains
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2 fibronectin type III domain
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PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
PROBABLE.
N-LINKED
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IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIERONECTIN TYPE-III 1.
FIERONECTIN TYPE-III 2.
HEPARIN-BINDING (POTENTIAL).
HEPARIN-BINDING (POTENTIAL).
                                                                                                                                                                     Score 223; DB
Pred. No. 3.1e-
57; Mismatches
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                                                                                                                                                                               223; DB 1;
No. 3.1e-08;
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(GLCNAC...)
(GLCNAC...)
(GLCNAC...)
(GLCNAC...)
(GLCNAC...)
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                                                                                                                                                                      150;
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(POTENTIAL).
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NESULT 14

NCM2 HA

AC 015394

AC
                 GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0007158; p:neuronal cell adhesion; TAS.
InterPro; IPR008957; FN III-ike.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR00358; Ig_cl.
InterPro; IPR00358; Ig_cl.
Pfam; PF00041; fn3; 2.
Pfam; PF00047; ig; 5.
SMART; SM00060; FM3; 2.
SMART; SM00060; FM3; 2.
SMART; SM000408; IGC2; 5.
SMART; SM000408; IGC2; 5.
Cell adhesion; Transmembrane; Glycoprotein; Repe
Immunoglobulin domain; Signal.
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015394;

15-JUL-1998 (Rel.

15-JUL-1998 (Rel.

10-OCT-0003 (Rel.

Neural cell adnes

NCAM2 OR NCAM21.
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Genew; HGNC:7657; NCAM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a copyre between the Swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.

MEDLINE-22660472; PubMedel12754519;
Zhang H., Li X.-J., Martin D.B., Aebersold R.;
"Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry.";
Nat. Biotechnol. 21:660-666 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paoloni-Giacobino A., Chen H., Antonarakis S.E.; "Cloning of a novel human neural cell adhesion molecule that maps to chromosome region 21q21 and is potentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC:
MIM; 602040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 43:43-51(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
MEDLINE=97369930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Down syndrome."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: May play important roles in selective from the primary olfactory subscitutary olfactory SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed most strongly in ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 5 immunoglobulin-like C2-type SIMILARITY: Contains 2 fibronectin type III domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM
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(Rel. 36, Last sequence update)
(Rel. 42, Last annotation update)
adhesion molecule 2 precursor (N-CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Human)
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  domain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9226371;
A., Chen H., An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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RESULT 15
NPHN MOUSE
ID NPHN MOUSE
AC Q9QZS7
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DT 28-FEB
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                                                                                                            VOTMVVLNNLEPNTTYEI
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                                                                                                                                                                                                                                                                                             KTDNGTYRCE-ASNIVGKAHSDYMLYVY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SM--PQKSFNATAERGEEMTFSCRASGS
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIBRONECTIN TYPE-II.
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Pred. No. 2.6e-08;
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CYTOPLASMIC (POTENTIAL).
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    MGD; MGI:185937; Nphs1.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007545; F:protein binding; IPI.
GO; GO:0007267; F:JNK cascade; IDA.
GO; GO:000165; P:MAPKXK cascade; IDA.
InterPro; IPR003957; FN III-like.
InterPro; IPR003951; FN III.
InterPro; IPR003959; ISI-like.
InterPro; IPR003959; ISI-like.
InterPro; IPR003599; ISI-like.
InterPro; IPR003599; ISI-like.
START; SM00401; fn3; 1.
SMART; SM00408; FN3; I.
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Cell adhesion; Transmembrane; Signal; Gl
 SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diaphragm, interacts with CD2AP and nephrin.
J. Clin. Invest. 108:1621-1629(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21590051; PubMed=11733379;
Shih N.Y., Li J., Cotran R., Mundel P.,
"CD2AP localizes to the slit diaphragm
novel C-terminal domain.";
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Nephrin precursor
NPHS1 OR NPHN.
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Abrahamson D.R
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Podocin, a raft-associated component of the glomerular
                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collabora-
ween the Swiss Institute of Bioinformatics and the EMBL outstati
European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 8 immunoglobulin-like domains. SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein (Potential) at podocyte slit diaphragm between podocyte foot processe TISSUB SPECIFICITY: Expressed in kidney glomeruli. PTM: Phosphorylated on tyrosine residues (By similarity). SIMILARITY: Belongs to the immunoglobulin superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Seems to play a role in the development or
the kidney glomerular filtration barrier. May anchor
slit diaphragm to the actin cytoskeleton.
SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP
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PubMed=10504499;
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Rodentia;
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CYTOPLASMIC (POTENTIAL)
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and binds to
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O9by67 homo sapien
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Q8x2f4 homo sapien
Q7tml1 mus musculu
Q86wb8 homo sapien
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1 MASVVLPSGSQCAAAAAAAAAPPGLRLRLLLLLESAAALIPTGDGQNLFTKDVTVIEGEVA 60 	Query Match 99.9%; Score 2280; DB 4; Length 442; Best Local Similarity 99.8%; Pred. No. 1.4e-186; Matches 441; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	Immunoglobulin domain. SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;	SMART; SM00408; IGc2; 1. PROSITE; PS50835; IG_LIKE; 3.	SM00294;	InterPro; IPR003585; Neurexin-like. Pfam: PF00047; ig: 3.	InterPro; IPR003598; Ig_c2.	InterPro; IPR007110; Ig-like.		SMBH: AF132811: AAF69029 1: -	to the ewel/General/Inet	of a novel human cDNA en	Zhou Y., Du G., Chen J., Yuan J., Qiang B.;	SEQUENCE FROM N.A.	[1]		Eukalyota; Metazoa; Chordata; Cianiata; veitebrata; Eutereostomi; Mammalia: Eitheria: Drimates: Catarrhini: Hominidae: Homo).			(TrEMBLrel. 25, Last	(TrEMBLrel. 17,	01-JUN-2001 (TrEMBLrel. 17, Created)	~	O9BY67 PRELIMINARY; PRT; 442 AA.	7 -

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                                                   Query Match
Best Local Sim
Matches 436;
                                                                                                                       Fukani T., Maryama T., Murakami Y.;

R Fukani T., Maryama T., Murakami Y.;

R Fukani T., Maryama T., Murakami Y.;

R Gobil CCT-2001 to the EMEL/GenBank/DDBJ databas

R EMBL, AF434663, AAL66736.1; -.

R MGD; MGI:1889272; Igsf4.

R GO; GO:0008021; C:synaptic junction; IDA.

R GO; GO:0008021; C:synaptic vestcle; IDA.

R GO; GO:0008121; C:synaptic vestcle; IDA.

R GO; GO:0008125; F:protein binding; IFI.

R GO; GO:0007155; F:protein binding; IFI.

R GO; GO:0007155; F:protein binding; IFI.

R GO; GO:0007167; P:synaptogenesis; IDA.

InterPro; IFR003158; Neurexin-like.

Pfam; PF00047; ig; 3.

SYART; SM00294; 4 1m; 1.

R PROSITE; PS080385; IG LIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEM
01-JUN-2002 (TrEM
01-OCT-2003 (TrEM
Tumor suprressor
                                                                                                    PROSITE; PS5083:
Immunoglobulin o
SEQUENCE 445 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8R4L1
Q8R4L1;
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                            STRAIN=129/SvJ;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGSF4.
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                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISCQVNKSDDSVIQLLNENRQTIYFRDERPLKDSRFQLLNESSSELKVSLTNVSISDEG
                MASVVLPSGSQCAAA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRAGEEGS IRAVDHAVIGGVVAVVVFAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTLTIITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNLNKTDNGTYRCEASNI VGKAHSDYML YVYDPPTTI PPPTTTTTTTTTTTTTL TI I TD
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  MASAVLPSGSQCAAAAAVAAAAAPPGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEG
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
essor in lung cancer 1.
                                                   98.2%;
larity 98.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                    AA; 48
                                                                                                                                                                                                                                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                     48664 MW;
                -AAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEG
                                                   1;
                                                  Score 2241.5; DB 1
Pred. No. 2.8e-183;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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databases.
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                                       Query Match
Best Local Similarity
Matches 434; Conser
                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; PP00047; Ig; 3.
SMART; SM00409; IG; 3.
SMART; SM00409; IGc2; 3.
SMART; SM00408; IGc2; 3.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain.
SEQUENCE 445 AA; 48666 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8K3T6
Q8K3T6;
01-OCT-2002
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                               "SynCAM, a synaptic
Science 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
STRAIN=C57BL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synaptic cell adhesion IGSF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biederer T.,
Sudhof T.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003
                                                                                                                                                                                                                                                                                                          IL; AF539424; AAN01614.1; -.

MGI:1889272; Igsf4.
GO:0045202; C:synaptic junction; IDA.
GO:008021; C:synaptic vesicle; IDA.
GO:0016347; F:calloium-independent cell adhesion molecule
GO:0016347; F:protein binding; IPI.
GO:0007515; F:cell adhesion; IDA.
GO:0007166; P:synaptogenesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
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  MASVVLPSGSQCAAA----AAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sara Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                             48666 MW;
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                                                               97.8%;
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                                           2;
                                           Score 2232.5; DB 1:
Pred. No. 1.7e-182;
2; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                             5B336F23F1877497 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kavalali E.T.,
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                                                                                     445;
                                           ω,
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                                                Gaps
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                                Query Match
Best Local Similarity
Matches 435; Conserv
                                                                                                                                          Submitted (JUN-2001) to the EMBL/GenBank/DDBJ EMBL; AB064265; BAB83501.2; -. MGD; MGI:1889272; Igsf4.

GO; GO:0045202; C:synaptic junction; IDA.
GO; GO:0005021; C:synaptic vesicle; IDA.
GO; GO:0006347; F:callcium-independent cell add.
GO; GO:0005155; F:protein binding; IPI.
GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:000715; P:synaptogenesis; IDA.
InterPro; IPR00710; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Neurexin-like.
Feam; PR00447; ig; 3.
SMART; SM00294; 4.lm; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 3.
Inmunoglobulin domath.
SEQUENCE 456 AA; 49787 MW; 3226E866A4BC1C
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IGSF4 OR RA175.
Mus musculus (Mouse).

Mukaryota; Metazoa; Chordata; C:

Bukaryota; Eutheria; Rodentia; S:

Mammalia; Eutheria; Rodentia; S:

NCBI TaxID=10090;
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8 Homo sapiens (Human).

1 Eukaryota; Metazoa; Chordata; Craniat Mammalia; Eutheria; Primates; Catarrh NCBI_TaxiD=9606;
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C Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K.
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K.
Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y

Nagahari K., Sugano S., Isogai T.;

"HRI human cDNA sequencing project.";

"Hayashi K., Nagai T., Nagai T., Nagai T., Nakamura Y.

"Hayashi K., Nagai T., Nagai T., Nagai T., Nakamura Y.

"Hayashi K., Nagai T., Nagai T., Nagai T., Nakamura Y.

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Pred. No. 4.1e-174;
4; Mismatches 20;
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01-OCT-2003 (TrEMBLrel. 25, Las)
01-OCT-2003 (TrEMBLrel. 25, Las)
01-OCT-2003 (TrEMBLrel. 25, Las)
Nectin-like molecule 2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
MCBI_TaxID=10090;
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Q7TNL1;
01-OCT-2003
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STRAIN-C57BL/6; TISSUE-Brain;
Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni
Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
"Implications of nectin-like molecule
2/IGST4/RA175/SgIGSF/TSLC1/SynCAM1 in cell-cell adhesion
transmembrane protein localization in epithelial cells.";
J. Biol. Chem. 0:0-0(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 0:0-0(2003).
EMBL; AY351388; AAQ02381.1; -.
SEQUENCE 417 AA; 45779 MW;
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  EVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN
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91.7%;
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Pred. No. 9.26
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Best Local Sim
Matches 331;
                                                                                                                                                                                                                                                                                                                                                                     Tto A., Koma Y., Nagano T.;

"Cloning of a secretory isoform of SqIGSF/TSLC-1.";

"Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; AB094146; BAC66178.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR007110; Ig-2.

R Pfam; PF00047; ig; 3.

R SMART; SM00409; IG; 3.

R SMART; SM00409; IG; 3.

R SMART; SM00409; IG; 3.

R PROSITE; PS50835; IG LIKE; 3.

SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q86WB8;
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01-JUN-2003 (TREMBLrel. 24, Last sequence update)
01-JCT-2003 (TREMBLrel. 25, Last annotation update)
Secretory isoform of TSLC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secretory isoform STSLC-1.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Lung;
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                                                                                                                                                                                                                                                                               1 MASVVLPSGSQCAAAAAAAAPPGLRLKLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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                NNLNKTDNGTYRCEASNIVGKAHSDYMLYVY
 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVY
                                                                  YKPQVHIQMTYDLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
                                                                                                                      KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
                                                                                                                                                           RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
                                                                                                                                                                         RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGBEIEVNCTAMASKPATTIRWF
                                                                                                                                                                                                              TISCOVNKSDDSVIQLLNPNROTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
                                                                                                                                                                                                                               TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
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                                                                                                       KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
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                                                                                                                                                                                                                                                                                                                     75.1%; Score 1715; DB 4; llarity 100.0%; Pred. No. 2.2e-138; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
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Best Loc
Matches
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Ito A., Koma Y., Nagano T.;
"A secretion form of SgIGSF/TSLC1.";
Submitted (SEP-2002) to the EMBL/GenBar
EMBL; AB092414; BAC66173.1; -
InterPro; IPR007210; Ig-like.
InterPro; IPR007210; Ig-like.
InterPro; IPR003599; Ig-c2.
Pfam; PF00047; Ig; 3.
SMART; SM00409; IG; 3.
                                                                                      O9D6E7;
O9D6E7;
O9D6E7;
O1-JUN-2001 (TrEMBLrel. 17, CO1-JUN-2001 (TrEMBLrel. 17, IO1-OCT-2003 (TrEMBLrel. 25, IO1-OCT-2003 (TrEMBLrel. 25, IO1-OCT-200073G06Rik protein. IGSF4 OR 2900073G06RIK. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        030VG4;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
A secretion form of SgTGSF/TSLC1.
             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A secretion to SSGIGSF/STSLC1
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Last sequence update)
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Pred. No. 1.1e
0; Mismatches
                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Sciurognathi; Muridae;
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RESULT Q9Z2H8 ID Q9 AC Q9 DT 01

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A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Aizawa K., Izawa M., Mishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Coasavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl R., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sokai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Buronstein M.J., Hoffmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Buzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilning L.,
Havashtaka Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 325
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EMBL; AKO13775; BAB23988.1; -.

MCD; MCD; MCB1:1889272; Igsf4.

GO; GO:0045202; C:synaptic junction; IDA.
GO; GO:0016324; F:calcium-independent cell adl
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007115; P:cell adhesion; IDA.
GO; GO:0007116; P:synaptogenesis; IDA.
GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR007110) Ig-like.
InterPro; IPR003598; Ig_c2.
Pfam; Pf00047; ig; 3.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain.
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STRAIN-C57BL/6J; TISSUE-Hippocampus;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wynshaw-Boris A
Hayashizaki Y.;
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STRAIN=C57BL/6J;
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SEQUENCE 336 AA;
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                     LFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVY
                                                                                                     EVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN
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LFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVY
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Pred. No. 1.2e-
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"Cloning of a novel cDNA encoding a member of ine
submitted (APR-1998) to the EMBL/GenBank/DDBJ dat
EMBL; AF061260; AAC67243.1; -

MCD; MCI:188272; Igsf4.

GO; GO:0045202; C:synaptic junction; IDA.
GO; GO:0016347; F:calcium-independent cell adhesi
GO; GO:000515; F:protein binding; IFI.
GO; GO:000715; P:cell adhesion; IDA.
GO; GO:0007145; P:synaptogenesis; IDA.
InterPro; IPR00359; Ig-1ike.
InterPro; IPR00359; Neurexin-like.
Fian; PF00047; ig; 2.

MART; SM00294; 4.lm; 1.

SMART; SM00408; IGC2; 1.

RPOSITE; PS0835; IG-LIKE; 2.

Immunoglobulin domain.
SEQUENCE 295 AA; 32509 MW; 9DE9D86F6FF6F488
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Best Local
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OL-MAY-2000 (TIEMBLIEL 1

OL-MAY-2000 (TIEMBLIEL 1

OL-CT-2003 (TIEMBLIEL 2

Adhesion protein RA175C.

IGSF4 OR RA175C.
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    Soyama
Momoi '
                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Mammalia; Eutheria;
                                             SEQUENCE FROM N.A
                                                                                   NCBI_TaxID=10090;
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                                                                                                         Craniata; Vertebrata; Sciurognathi; Muridae;
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ database
RMBL, AB021066; BAR87916.1; -
RMBL; MB021066; BAR87916.1; -
RMBL; MGD; MGI:1889272; Igsf4.
GG; GG:0045202; C:synaptic junction; IDA.
GG; GG:0008021; C:synaptic vesicle; IDA.
GG; GG:0008021; C:synaptic vesicle; IDA.
GG; GG:00015347; F:calcium-independent cell adhesion mo
GG:00007155; F:cell adhesion; IDA.
GG; GG:0007156; P:synaptogenesis; IDA.
GG:0007166; P:synaptogenesis; IDA.
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Best Local Similarity
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003595; Neurexin-like.
Pfam; PF00047; ig; 2.
SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 2.
Immunoglobulin domain.
SEQUENCE 306 AA; 33522 MW; A4CE37
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QYL6;
Q9QYL6;
01-MAY-2000
Soyama A., Fujita E., Urase K., Mukasa T., Kourok Momoi T.;

"RA175, a novel neuron specific adhesion protein. Submitted (DEC-1998) to the EMBL/GenBank/DDBJ dat EMBL; AB021964; BAA87914.1; -.

MGD; MGI:1889272; Igsf4.

GO; GO:0045202; C:synaptic junction; IDA.

GO; GO:0008921; C:synaptic vesicle; IDA.

GO; GO:0016347; F:calcium-independent cell adhesi.
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01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Adhesion protein RA175A.
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Mammalia; Eutheria;
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IGSF4 OR RA175A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYVYDPPTTIPPPTTTTTTTTTTTILTIITDTTATTEPAVHDSRAGEEGTIGAVDHAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYPCEASNIVGKAHSDYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVH1QMTYPLQGLTREGDALELTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                            (Mouse).
etazoa; Chordata;
theria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306
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13,
25,
                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence up
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Pred. No. 2.5e-120;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; 1
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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on update)
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       adhesion molecule
                                                                                                                                                                                                   Kouroku
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                                                                                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                                                                     Momoi
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          IDA.
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Best Local Sim
Matches 283;
WARAITS, a novel neuron specific adhesion pr

Submitted (DEC-1998) to the EMBL/GenBank/DI

Submitted (DEC-1998) to the EMBL/GenBank/DI

EMBL; AB021965; BAA67915.1; -.

MGD; MGI:1889272; Igsf4.
GO; GO:0045202; C:synaptic junction; IDA.
GO; GO:0016347; F:calcium-independent cell
GO; GO:0016347; F:calcium-independent cell
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007155; P:cell adhesion; IDA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003589; Ig_c2.
InterPro; IPR003585; Neurexin-like.
Pfam; PF00047; 19; 2.
SMART; SM00408; IGc2, 1.
PROSITE; PS50885; IG LIKE; 2.
Inmunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007415; P:cell adhesion; IDA.
GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Neurexin-like.
PROSTOR; SM00294; 4.1m; 1.
SMART; SM00408; IGc2; 1.
PROSTOR; DE50835; IG LIKE; 2.
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Q9QYL5;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-CCT-2003 (TrEMBLrel. 2
Adhesion protein RA175B.
IGSF4 OR RA175B.
                                                                                                                                                                                                                                                                                                                                                                                             idhes....
IGSF4 OR RA1756.
Mus musculus (Mouse).
Mesazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                        Soyama A
Momoi T.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
[1]
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SEQUENCE 295 AA; 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTC
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                                                                                                                                                                                                                                                                                                                                         [F]
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                                                                                                                                                                                                                                                                                                                                         Urase
                                                                                                                                                                                                                                                                                  specific adhesion protein.";
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13,
25,
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Last sequence up
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Pred. No. 1.4e
3; Mismatches
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                         Mukasa
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                                                                                                                                                                                                  cell adhesion
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                                                                                                                                                                                                                                                                                                                                         Kouroku
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                                                                                                                                                                                                  molecule
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Murinae; Mus
                                                                                                                                                                                                                                                                                                                                           Momoi
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Query Match
Best Local Simi
Matches 271;
                                                                                                                                                                        A Momoir:;

RA175, a novel neuron specific adhesion protein.";

RA175, a novel neuron specific adhesion protein.";

Submitted (DCC-1998) to the EMBL/GenBank/DDBU database REMEL; AB021967; BAA87917.1;

RMGD; MGI:1889272; Igsf4.

RGO; GO:0045202; C:synaptic vesicle; IDA.

RGO; GO:0045202; C:synaptic vesicle; IDA.

RGO; GO:0000521; C:synaptic vesicle; IDA.

RGO; GO:00005215; F:calcium-independent cell adhesion mo RGO; GO:0007155; F:calcium-independent cell adhesion mo RGO; GO:0007155; F:cell adhesion; IDA.

RGO; GO:0007155; P:cell adhesion; IDA.

RGO; GO:000716; P:synaptogenesis; IDA.

RGO; GO:000716; 
                                                                                          Query Match
Best Local S
Matches 266
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01-MAY-2000 (TrEMBLrel. 1
01-OCT-2003 (TREMBLrel. 2
Adhesion protein RA175N.
IGSF4 OR RA175N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QYL3;
Q9QYL3;
01-MAY-2000
01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                                                                                                    Similarity
                                    MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQLML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIDIQKDTAVEGBEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQLML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYM
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nilarity 90.2%;
Conservative
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Rodentia;
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Pred. No. 5.6e
3; Mismatches
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5.4e-109;
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KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTC

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TISSUE-Amygdala;
Koehrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL834270; CAD38945.1; -.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.
R InterPro; IPR003599; Ig.-c2.
R Ffam; PF00047; ig; 3.
R Pfam; PF00047; ig; 3.
R SMART; SM00409; IG; 2.
R PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50835; IG_LIKE; 3.
W Hypothetical protein; Immunoglobulin domain.
W SEQUENCE 435 AA; 47554 MW; 59DDD41B7F34D446 CRC64;
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Matches 1
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8N3J6;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWS----DMYTVTSQ 204
                                                                                                                                                                                                                                                         DFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNL 147
                           AHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTT-------DSRAGEEG
                                                     ILTCESKGKPLPEFVLWTKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCEATNTIGO
                                                                           ELTCEAIGKPQPVNVTWVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGK 321
                                                                                                             LMLKVHKEDDGVPVICQVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDAL 263
                                                                                                                                                                         QISGFSSPVMEGDLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSST 187
                                                                                                                                                                                                                                DKKALRDNRIELVRASWHELSISVSDVSLSDEGQYTCSLFTMPVKTSKAYLTVLGVPEKP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLCILIIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
SSAEYVLIVHDVPNTLLPTTIIPSLTTATVTTTVAITTSPTTSATTSSIRDPNALAGONG
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Search completed: July 7, 2004, 06:02:44 Job time : 64.8289 secs

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Database :
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Maximum DB
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1: geneseqp1980s:*
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25-MAY-2000.

27-OCT-1999; 99WO-US025031.

28-OCT-1998; 98US-0105971P.

(HUMA-) HUMAN GENOME SCI INC.

Ni J, Ruben SM, Greene JM; Olsen HS, Young PE, Kenny JJ, Moore PA, Wei Y;

Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases. WPI; 2000-387742/33.

Disclosure; Page 182-183; 803pp; English.

The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences give AAAB0606-AB0623 encode the 12 secreted protein sequences given in AAB25576-B25593. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the given ä.

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                                                    Human; HCSRP; cytostatic; antiarthritic; antirheumatic; antiasthmatic; immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic; neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia;
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Tang YT,
Hillman
    New human cell surface receptor protein and polynucleotide useful diagnosis, prevention and treatment of cancer, immune disorders, infection and neuronal disorders.
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Lymphoid derived dendritic cell B7-L1; T cell proliferation; nat

natural

adhesion molecule; LDCAM; human; B7-1; tural killer cell; NK; tumour cell;

Query Match
Best Local Similarity
Matches 442; Conserv

100.0%; Score 2283; DB 3; ilarity 100.0%; Pred. No. 5.8e-158; Conservative 0; Mismatches 0;

Length

442; 0

Gaps

0

Sequence

442

A

Human lymphoid derived dendritic cell adhésion molecule.

31-MAY-2000

(first entry)

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The present amino acid sequence is the human lymphoid derived dendrtitic cells adhesion molecule, LDCAM. It is found on lymphoid derived dendrtitic cells and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-11. Human LDCAM is expressed in breast, retina, foetal liver, spleen and heart, lung, muscle, placenta, thyroid and lung carcinoma. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B71-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of organ and bone marrow transplant rejection and for modulating T cells immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or cells bearing B7L-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 42-43; 44pp; English
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 The invention relates to disorder associated with
                                          Disclosure; Page 49-50; 59pp; English
                                                                      TSLC1 level.
                                                                                 Detecting cell proliferative disorder associated with tumor suppressor lung cancer (TSLC) 1 in subject, comprises contacting proliferating ce of subject with reagent detecting TSLC1 and detecting modification in
                                                                                                                                                                        Reeves RH,
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                                                                                                                                                                                                                                                          15-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Human tumour
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a method for detecting cell proliferative tumour suppressor lung cancer 1 (TSLC1) is
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Matches 442
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                                                                  SRAGEEGS TRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA
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ABP62825 standard; protein; 442 ጀ

ABP62825;

14-OCT-2002 (first entry)

Human polypeptide SEQ IJ NO 262.

RESULT 5
ABP628A
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XX ABP6
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XX HOMO Human; vulnerary; dermatological; neuroprotective; nootropic; can antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue r burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy. cancer;

Homo sapiens

WO200218424-A2

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Zhao
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Mismatches 0;
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The invention relates to an isolated nucleic molecule that is at least CC 95% identical to 18 human cDNA sequences representing 12 novel genes CC encoding secreted proteins or a polynucleotide fragment of the cDNA Sequence contained in American Type Culture Collection (ATCC) deposit No. CC defined in the specification, its species homologue, a variant or allelic variant of the polynucleotide having a polynucleotide capable of CC hybridising under conditions the polynucleotide, where the polynucleotide does not hybridise under stringent conditions to a nucleic acid molecule CC having a nucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polypeptide), the CC secreted polypeptide (comprising a sequence that is at least 95% CC identical to a polypeptide fragment, domain, epitope, full-length CC protein, variant, allalic variant or species homologue), antibodies that specifically bind to the polypeptides, diagnosing, treating, preventing or ameliorating a medical condition by administering the polypucleotide (or the polypeptide, the gene corresponding to the cDNA sequence and conditions to a nactivity in a biological assay (by expressing an activity
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18-APR-2001;
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27-OCT-1999;
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RUBEN S M.
LIU D.
CROCKER P R
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M, Liu D,
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KENNY JJ.
OLSEN HS.
MOORE PA.
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2001US-00836353.
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Crocker PR;
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Best Local Simi
Matches 442;
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                                                                                                                                                                                                                                                                 Human Protein
                               WO2003016475-A2
                                                                                          Homo
                                                                                                                                                                                                                                                                                                                            29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                       ADE54238
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                                                                                                                                           pain; neuronal tissue; gene therapy;
segmental nerve injury; chronic constriction injury; CCI;
nerve injury; SNI; Chung.
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Pred. No. 5.8e-158;
Mismatches 0;
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Comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially cexpressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity in an animal of one or more small molecule that regulates the activity in an animal of one or more of the polypeptides given in the composition and a pharmaceutical composition comprising the one or more of polypeptides or their antibodies. The polynucleotide or the compound that composition comprising the one or more of injury (CCI) and spared nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (SNII) in an animal (e.g. gene conjurce data for this patent did not form part of the printed conformation, but was obtained in electronic form directly from WIPO at the specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention discloses a composition comprising two or more or human polynucleotides or a polynucleotide which represents derivative or allelic variation of the nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New composition comprising preparing a medicament for
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                     specification, but was obtained in electr
ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page; 1017pp;
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GENBANK; NP_055148.
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BAYER AG:
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Sequence 442 AA;

Similarity

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Length

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Query Match
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                                                                                                                                                                                     TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
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                                                                                                                                                                                                                                                         MASVVLPSGSQCAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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                                                 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
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ilarity 100.0%;
Conservative (
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Query Match
Best Local Similarity
                                                      disorders
the amino
                                                                        preparing condition
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27-OCT-1999;
19-APR-2000;
                                                                                                                                              New nucleic acid molecule, useful for preventing, treating or ameliorating liver disorders or neural disorders.
                                                                                                                                                                                                                               (WEIY/)
(GREE/)
(RUBE/)
                                                                                            domain,
                                                                                                  allelic
                                                                                                                           Disclosure; SEQ ID NO 136; 380pp; English.
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                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                          secreted presents disorder;
                                                   ention relates to an isolated nucleic acid sequence, or its variant, a fragment of the cDNA sequence, or its fragment, epitope or species homologue. The nucleic acid is useful for new a medicament for preventing, treating or ameliorating a medical on e.g., cancer, liver disorders such as hepatitis or neural rs such as Alzheimer's disease. The present sequence represents no acid sequence of a novel human secreted protein associated
                                                                                                                                                                                                                              GREENE J M.
RUBEN S M.
                                                                                                                                                                                                                                               YOUNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
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99WO-US025031.
2000US-0198407P.
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Alzheimer's disease.
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No. 5.
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                                                                                                                                                        preparing
medical
                                                                                                                                                                                                                                                                                                                                                                                                                                  disorder;
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DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
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                                                                                                                                                     g a medicament condition e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatitis;
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         442;
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                                                                                                                                                       for cancer,
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                                                                                                                         05-JUN-2001;
10-OCT-2001;
15-FEB-2002;
Identifying modulators of the p53 pathway for use in or cell proliferation disorders, comprises screening modulate activity of a human ortholog of genes that m pathway in Drosophila.
                                                                                                                                                                                                                                                  antiapoptotic; p53 pathway; breast
lung cancer; ovarian cancer; angio
apoptotic disorder; cell prolifera
                                                                                                                                                                    03-JUN-2002; 2002WO-US017382.
                                                                                                                                                                                                            WO200299122-A1
                                                                                                                                                                                                                                                                                Human; p53 modifier;
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                                                                                                                                                                                                                                                                                                                                                 ABC07196;
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                                                                                                                                                                                         12-DEC-2002
                                                                                                                                                                                                                                 Homo
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                                                   2003-156859/15.
DB; ACD13371.
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                                                                                                      EXELIXIS
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                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                                                                                                         2001US-0296076P
2001US-0328605P
2002US-0357253P
                                                                                  Plowman
                                                                                                                                                                                                                                                                                                                           (first
                                                                                                       INC
                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                   cell proliferation
                                                                                                                                                                                                                                                                                                                            entry)
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breast cancer; colon cancer; kidney ca
angiogenesis; cell cycle;
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                                                                                 Francis-Lang
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modify the p53
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Example

2; Page 469-470;

678pp; English

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CC The invention relates to identifying (MI) a candidate p53 pathway CC modulating agent, by contacting an assay system comprising a purified HM CC polypeptide (human orthologue of genes that modify the p53 pathway in CC Drosophila) or nucleic acid with a test agent under conditions, where but CC contacting or nucleic acid with a test agent under conditions, where but CC contacting a cell defecting a test agent biased activity of the assay system. CC Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator CC that specifically binds on HM polypeptide comprising an HM maino acid CC sequence, where p53 function is restored), modulating (M3) a p53 pathway CC in a mammalian cell (comprising contacting the cell with an agent that Specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) CC adisease in a patient (comprising contacting the sample with a probe for HM comparing the results with a control, and (d) determining CC expression; (d) comparing the results with a control, and (d) determining contacting the p53 pathway. A probe for HM expression cis useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 * expression level. CC modulations where disease or disorder prognosis is related to defects in the p53 pathway, such as angiogenesis, apoptotic or cell proliferation of the cell, so that the cell undergoes normal couseful for modulating the p53 pathway of a cell, thus restoring consecuted a lower of the cell, thus restoring the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring consecutes a lower of the cell undergoes normal consecutes a lower of the cell undergoes normal consecutes a lower of the cell proliferation disorders. The present sequence consecuted the p53 pathway and a cell to contact sequence consecuted the p53 pathway and cell to cell the cell contact sequence cell contact sequence cell contact sequence cell
Sequence 442 AA;
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₩Db 밁 Ş Ş B Ś Š 밁 Ş 밁 Query Match
Best Local Similarity
Matches 441; Conserv 241 241 181 181 121 121 61 61 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAVASKPATTIRWF TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG MASVVI.PSGSQCAAAAAAAAPPGLRIRILLLLIFSAAAIIPTGDGQNIFTKDVTVIEGEVA YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQRDTAVEGEEIEVNCTAMASKPATTIRWF TISCQVNKSDDSVIQLLNENRQTIYFRDFRELKDSRFQLLNFSSSELKVSLTNVSISDEG MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ Conservative 99.9%; Score 2280; DB 6; Pred. No. 9.6e-158; 1; Mismatches 0; Length 442; Indels 0; 240 300 180 120 120 60 240

δ 유정 Ś 밁 吊 301 421 361 361 301 421 NNI.NKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTILTIITD SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA NNLNKTDNGTYRCEASNI VGKAHSDYMLYVYDPPTTI PPPTTTTTTTTTTTTTTLTI I TD DTAIINAEGGONNSEEKKEYFI 442 420

> ABO07231 standard; protein; 442 ጅ

13-AUG-2003 (first entry)

ABC07231;

Human p53 modifying protein, SEQ ID 191

Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.

Homo sapiens.

W0200299122-A1

12-DEC-2002

03-JUN-2002; 2002WO-US017382.

05-JUN-2001; 2001US-0296076P. 10-OCT-2001; 2001US-0328605P. 15-FEB-2002; 2002US-0357253P.

(EXEL-) EXELIXIS INC

Friedman L, Plowman ନ Belvin M, Francis-Lang ä Ľ Ď Funke RP;

WPI; 2003-156859/15. ACD13404.

Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.

Example 2; Page 557-559; 678pp; English

ABOO7231
IID ABOO7231
XX
XX
AC ABOO
XX
XX
AC ABOO
XX
XX
Huma
X CC The invention relates to identifying (M1) a candidate p53 pathway CC modulating agent, by contacting an assay system comprising a purified HM CC polypeptide (human orthologue of genes that modify the p53 pathway in CC posophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference cartivity, and detecting a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent with a candidate modulator CC in a contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid CC in a mammalian cell (comprising contacting the cell with an agent that compectively) binds an HM polypeptide or nucleic acid) and diagnosing (M4) candidate modulator; (c) comparising contacting the control; and (d) determining CC expression; (c) comparing the results with a control; and (d) determining CC expression; (c) comparing the results with a control; and (d) determining considered the comparison indicates a likelihood disease). (M1) is useful considered to diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 * expression level conditations, where disease or discorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation of the cell, so that the cell undergoes normal consideration or progression through the cell undergoes normal consideration or cell proliferation discorders. The present sequence consideration or cell proliferation discorders. The present sequence

Sequence

99.98; Score 2280; 몂 6 Length 442;

RESULT 10

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RESULT 11
ADE61605
ID ADE61
XX ADE61
XX ADE61
XX Humar
XX Humar
XX Humar
XX Humar
XX Humar
XX Homo
DE HOMO
XX HOMO
YX 
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01-NOV-2001;
26-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human;
spinal
                       New composition comprising two or more isolated polypeptides, preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2004
                                                                                               WPI; 2003-268312/26.
GENBANK; AAF69029.
                                                                                                                                                                        Woolf
                                                                                                                                                                                                                      (GEHO )
(FARB )
                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pain; neuronal tissue; gene therapy; segmental nerve injury; chronic cons nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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2001US-0346382P.
2001US-0333347P.
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01-NOV-2001;
26-NOV-2001;
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                                                                                                                                                         Sequence
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                                                                                        Goddard A,
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97US-0067411P. PRO 322
97US-006973P. PRO 749
97US-0069334P. PRO 749
97US-0069334P. PRO 749
97US-0069694P. 742
97US-0069694P. 747
97US-0069694P. 747
97US-00696970P. 747
97US-006970P. 747
97US-006970P. 747
97US-006970P. 747
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98US-0074086P.
98US-0074092P.
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                                                                                           Baker KP,
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Best Local S
Matches 440
                                                                                                                        PRO715;
PRO361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
   Modified-site
                                                                                                        detection;
                                                                                                                                                                                   Human
                                                                                                                                                                                                                25-SEP-2000
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                              Peptide
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                                                                                                    mbrane bound protein; secreted protein; PRO357; PRO327; PRO3241; PRO323; PRO299; PRO233; PRO344; PRO347; PRO355; PRO365; transmembrane polypeptide; antibody; screening; on; inhibition; probe; primer; human.
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 1. .36
/label=
9. .15
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Pred. No. 1.7e
0; Mismatches
                peptide
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..7e-156;
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01-DEC-1998;
16-DEC-1998;
22-DEC-1998;
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Gerritsen
Hillan KJ,
                                                                                                                      New human
which are
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/note= "N
428. .432
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/note= "N-
402. .408
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430. .4
/note=
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307. .313
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163. .167
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which are designated as PRO polypeptides are described The membrane-bo proteins have various industrial applications, including as pharmaceutical and diagnostic agants. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
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98US-0112850P.
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Roy MA, Tumas D, Wood WI;
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01-DEC-2000; 2000WO-USC3332B.
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Baker : Pan J, KP, Smith Chen J with V, ۲, Watanabe Desnoyers L, Goddard A, G atanabe CK, Wood WI, Zhang Godowski Ľď, Gurney ĀĿ;

N-PSDB; AAS45941. 2001-602746/68.

Novel nucleic acids encoding PRO polypeptides, used presence of tumors, such as prostate and breast tumoscreen for modulators of the compounds. tumors, ő diagnose the and ď

Claim 11; Fig 34; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.

CC The PRO polypeptides and their associated nucleic acids can be used to compete the presence of a tumour in a mammal by comparing the level of capression of a PRO polypeptide in a test sample of cells from the animal cexpression of a PRO polypeptide in a test sample of cells from the animal capression in the test sample includes the presence of a tumour in the capression of the test sample includes the presence of a tumour in the capression in the test sample includes the presence of a tumour in the capression of the presence of a tumour in the capression of the presence of a tumour in the capression of rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNP) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO contacted contacted with it. A specific polypeptide can be used to stimulate the prosence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, the proliferate, rectal, cervical, or liver tumours, in mammalian color, can be used for genetic analysis of individuals with genetic disorders and be used for genetic analysis of individuals with genetic disorders.

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Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-944-93-61 US-09-944-432-61 US-09-944-433-61 US-09-944-433-61 US-09-944-433-61 US-09-944-896-61 US-09-944-896-61 US-09-944-896-61 US-09-944-903-61 US-09-944-903-61 US-09-944-903-61 US-09-945-584-60 US-09-945-584-60 US-09-945-584-62 US-10-201-858-3 2 US-10-201-858-3 2 US-10-201-858-3 2 US-10-201-858-3 2 US-10-201-858-3 2 US-10-201-873-3 2 US-10-201-873-3 2 US-10-174-483-3 2 US-10-176-915-3 2 US-10-176-915-3 3 US-10-176-915-3 3 US-10-176-915-3 2 US-10-176-915-3 3 US-10-176-915-3 3 US-10-176-915-3
-09-944-396-61 -09-944-432-61 -09-944-654-61 -09-944-614-61 -09-944-896-61 -09-944-896-61 -09-944-896-61 -09-944-896-61 -09-944-896-61 -09-944-896-61 -09-944-896-61 -09-944-896-61 -09-944-896-61 -09-944-896-66 -09-944-896-66 -09-944-896-66 -09-945-580-67 -09-945-580-67 -09-945-580-3 -10-201-858-3 -10-201-858-3 -10-201-858-3 -10-176-916-858-3 -10-176-916-93 -10-176-916-3 -10-176-916-3 -10-176-916-3 -10-176-916-3 -10-176-916-3 -10-176-916-3

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CCURRENT APPLICATION NUMBER: US/09/778,510
CCURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1990-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SODTWARE: PATENTIN Ver. 2.0
SEQ ID NO 20
LENGTH: 442
TYPE: PRT
ORGANISM: Homo Bapien
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Best Local 9
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                                                                                           TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
                                                                                                                                            MASVVLPSGSQCAAAAAAAAPPGLRLLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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100.0%; Pred. No. 9.1e-177;
tive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/778,1878
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: PCT/US99/17905
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR PILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-778-187B-2
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Best Local Similarity
Matches 442; Conserv
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Patent NO. US2002018712A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow III, William C
TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILE REFERENCE: 2873-US
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 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
                              NNLNKTONGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTLTIITI
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US-09-984-130-136
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PRIOR FILLING DATE: 2000-10-30
PRIOR PELICATION NUMBER: 09/836,353
PRIOR PELICATION NUMBER: 09/836,353
PRIOR PELICATION NUMBER: 60/198,407
PRIOR PELICATION NUMBER: FCT/US99/25031
PRIOR PELICATION NUMBER: PCT/US99/25031
PRIOR PELICATION NUMBER: 60/105,971
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Best Local S
Matches 442
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Publication No. US20030055231A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
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SEQ ID NO 136
LENGTH: 442
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DTAIINAEGGONNSEEKKEYFI 442
                                                                         SRAGEEGS I RAVDHAVI GGVVAVVVFAMLCLL I I LGRYFARHKGTYFTHEAKGADDAADA
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Pred. No. 9.1e-177;
Mismatches 0;
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FILE REFERENCE: FF489F1
CURRENT APPLICATION NUMBER: US/09/836,353A
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 2000-04-19
PRIOR PELICATION NUMBER: 60/198/25031
PRIOR EILING DATE: 1999-10-27
PRIOR PILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR PILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 136
LENGTH: 442
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US-10-363-616-262
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US-09-836-353A-136
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Publication No. US20030129685A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
Sequence 262, Application US/10363616
publication No. US20040044181A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION UNMERE: 09/654,935
PRIOR APPLICATION UNMER: 09/654,935
PRIOR FILING DATE: 2000-09-01
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Best Local :
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                                                                  TYPE: PRT
ORGANISM: Homo sapien
US-10-302-041-20
                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/302,041
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/778,510
PRIOR FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER: OF SEQ ID NOS: 22
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SEQ ID NO 262
LENGTH: 442
TYPE: PRT
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Best Local Similarity
Matches 442; Conserv
Query Match 100.0%; Score 2283; DB 14; Best Local Similarity 100.0%; Pred. No. 9.1e-177; Matches 442; Conservative 0; Mismatches 0;
                                                                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                         APPLICANT: Baum, Peter TITLE OF INVENTION: Molecules Designated FILE REFERENCE: 2844-US
                                                                                                                      LENGTH: 442
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Pred. No. 9.1e-177;
D; Mismatches 0;
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Sequence.1, Application US/10403107

Publication No. US20030165974A1

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: REFUES, ROGET
APPLICANT: YOSHINORI, MUTAMAKİ
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSO
FILE REFERENCE: JHU1770-1
CURRENT APPLICATION NUMBER: US/10/403,107
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US/09/930,803
PRIOR APPLICATION NUMBER: US/09/930,803
PRIOR APPLICATION NUMBER: US/09/930,803
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0

LENGTH: 403

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US-10-403-107-1
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                              tch 100.0%; Score 2283; DB 14; al Similarity 100.0%; Pred. No. 9.1e-177; 442; Conservative 0; Mismatches 0;
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                        KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
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CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR TILING DATE: 2000-11-7
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR APPLICATION NUMBER: 60/309,261
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NUMBER OF SEQ ID NOS: 205
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 111
LENGTH: 442
                                                                                                                   Query Match
Best Local Similarity
Matches 442; Conserv
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Shenoy, Suresh G
Spytek, Kimberly A
Zerhusen, Bryan D
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Shimkets, Richard A
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                                                                                                                   100.0%; Score 2283; DB 15; ilarity 100.0%; Pred. No. 9.1e-177; Conservative 0; Mismatches 0;
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APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
MASVVLPSGSQCAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
                       MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLESAAALIPTGDGQNLFTKDVTVIEGEVA 60
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CURRENT APPLICATION NUMBER: US/10/015,115

CURRENT APPLICATION NUMBER: 007-9-23

PRIOR APPLICATION NUMBER: 60/248,153

PRIOR PILING DATE: 2000-11-13

PRIOR PPLICATION NUMBER: 60/249,598

PRIOR PILING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 60/264,240

PRIOR PILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/266,127

PRIOR APPLICATION NUMBER: 60/269,562

PRIOR PILING DATE: 2001-02-02

PRIOR PILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: 60/309,361

PRIOR APPLICATION NUMBER: 60/309,361

PRIOR APPLICATION NUMBER: 60/309,361

PRIOR APPLICATION NUMBER: 60/309,261

PRIOR APPLICATION NUMBER: 60/309,261

PRIOR APPLICATION NUMBER: 60/309,261

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2001-07-31
                                                                     PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 110
LENGTH: 442
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Publication No. US20030207800A1
GENERAL INFORMATION:
TYPE: PRT
ORGANISM: Homo sapiens
-10-015-115-110
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APPLICANT:
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APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
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APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides
TITLE OF INVENTION: Using the Same
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Shimkets, Richard A
Taupier, Raymond J
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or f
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
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US-09-866-028-61
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; ORGANISM: Homo Sapien US-09-866-028-61
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GENERAL INFORMATION
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APPLICANT: Eaton
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5. US20020058309A1
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Tumas, Daniel
Wood, William
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Godowski, Paul
Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
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Napier, Mary
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Hillan, Kenneth
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Pred. No. 1.6e-176;
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Query Match

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RESULT 11
US-09-944-449-61
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                                                                                                                                                                     TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P254891C1
CURRENT APPLICATION NUMBER: US/09/944,449
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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OR APPLICATION NUMBER: 60/067,411
OR FILING DATE: December 3, 1997
OR APPLICATION NUMBER: 60/069,334
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069335
OR FILING DATE: December 11, 1997
OR APPLICATION NUMBER: 60/069,278
OR APPLICATION NUMBER: 60/069,278
OR APPLICATION NUMBER: 60/069,425
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Tumas, Daniel
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Hillan, Kenneth
Kljavin, Ivar
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Goddard, Audrey
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; ORGANISM: Homo
US-09-944-449-61
                                                                                             ; NUMBER OF SEC
; SEQ ID NO 61
LENGTH: 440
    Query Match
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IOR APPLICATION NUMBER: December 1, 1998
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TOP FILING DATE: December 16, 1998
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CR FILING DATE: February 9, 1998
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COR FILING DATE: February 25, 1998
COR FILING DATE: February 25, 1998
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COR FILING DATE: December 16, 1998
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COR APPLICATION NUMBER: 60/113,296
COR FILING DATE: December 22, 1998
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COR FILING DATE: December 22, 1998
COR FILING DATE: July 28, 1999
COR FILING DATE: July 28, 1999
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COR APPLICATION NUMBER: 60/146,225
COR FILING DATE: July 28, 1999
COR APPLICATION NUMBER: 607/16,19330
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APPLICATION NUMBER: 09/254,311
FILING DATE: March 3, 1999
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APPLICATION I
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NUMBER: 6
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NUMBER: PCT/US00/05841
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NUMBER: 60/068,017
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NUMBER: PCT/US00/04414
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NUMBER: PCT/US00/03565
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P25481C1
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/86,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR RELING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/667,411
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
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PRIOR APPLICATION NUMBER: 60/069,425
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Patent No. Haker, K
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US-09-944-457-61
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APPLICANT: Baton, I
APPLICANT: Ferrar
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Roy, Margaret
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Gurney,Austin
Hillan,Kenneth
Kljavin,Ivar
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Goddard, Audrey
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Filvaroff, Ellen
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                                                                  PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILLING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILLING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILLING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-457-61
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PRIOR PILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR PILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR PILING DATE: March 3, 1999
PRIOR PILING DATE: March 3, 1999/1252
PRIOR PILING DATE: More 22, 1999
PRIOR PILING DATE: Junne 27, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: NO. US20020110859Alember 30, 199
PRIOR PILING DATE: NO. US20020110859Alember 30, 199
PRIOR PILING DATE: NO. US20020110859Alember 30, 199
PRIOR PILING DATE: December 1, 1999
PRIOR PILING DATE: DECEMBER: PCT/US99/28301
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR PILING DATE: February 11, 2000
PRIOR PILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
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PRIOR PILING DATE: December 16, 1997
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PRIOR PILING DATE: December 18, 1997
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PRIOR PILING DATE: PEDVIARY 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR PILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/113, 296
PRIOR PILING DATE: December 16, 1998
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PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
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APPLICANT: Grimaldi, Christopher
APPLICANT: Grimaldi, Christopher
APPLICANT: Hillan, Kenneth
APPLICANT: Hillan, Kenneth
APPLICANT: Njavin, Ivar
APPLICANT: Najavin, Ivar
APPLICANT: Nod, Milliam
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLCI
CURRENT APPLICATION NUMBER: US/09/944,862
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069335
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Godowski, Paul
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                                                                           PRIOR APPLICATION NUMBER: PCT/US00/32678

PRIOR FILING DATE: December 1, 2000

PRIOR FILING DATE: February 28, 2001

NUMBER OF SEQ ID NOS: 120

SEQ ID NO 61

LENGTH: 440

TYPE: PRT

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IOR APPLICATION NUMBER: 09/216,021
IOR APPLICATION NUMBER: 09/216,517
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IOR APPLICATION NUMBER: 09/254,311
IOR FILING DATE: December 22, 1998
IOR APPLICATION NUMBER: 09/254,311
IOR FILING DATE: Warch 3, 1999
IOR APPLICATION NUMBER: PCT/US99/1252
IOR FILING DATE: Unit 22, 1999
IOR APPLICATION NUMBER: PCT/US99/21090
IOR FILING DATE: September 15, 1999
IOR APPLICATION NUMBER: PCT/US99/28313
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IOR APPLICATION NUMBER: PCT/US99/28310
IOR APPLICATION NUMBER: PCT/US99/3301
IOR APPLICATION NUMBER: PCT/US99/3301
IOR APPLICATION NUMBER: PCT/US99/33095
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COR FILING DATE: February 25, 1998

COR FILING DATE: February 25, 1998

COR FILING DATE: December 16, 1998

COR FILING DATE: December 22, 1998

COR FILING DATE: December 22, 1998

COR FILING DATE: JOHNEER: 60/113,296

COR FILING DATE: JOHNEER: 60/146,222

COR FILING DATE: JOHNEER: FOT/US98/19330

COR FILING DATE: September 16, 1998

COR FILING DATE: September 16, 1998

COR APPLICATION NUMBER: FOT/US98/25108

COR FILING DATE: September 1, 1998

COR APPLICATION NUMBER: FOT/US98/25108

COR FILING DATE: December 1, 1998

COR APPLICATION NUMBER: POT/US98/25108

COR PILING DATE: December 1, 1998

COR PILING DATE: DECEMBER: POT/US98/25108
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R APPLICATION N
R FILING DATE: I
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APPLICATION NUMBER: PCT/US00/20710
FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
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APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
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APPLICATION NUMBER: PCT/US00/05841
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FILING DATE: February 11, 2000
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APPLICATION NUMBER: 60/068,
FILING DATE: December 18, 1
APPLICATION NUMBER: 60/070,
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APPLICATION NUMBER: PCT/US00/04414
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Length 440;
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/66,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,353
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PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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           Query Match
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ICR FILING DATE: JULy 28, 1999

ICR FILING DATE: September 16, 1998

ICR FILING DATE: September 16, 1998

ICR FILING DATE: December 16, 1998

ICR FILING DATE: December 1, 1998

ICR FILING DATE: December 16, 1998

ICR FILING DATE: December 16, 1998

ICR APPLICATION NUMBER: 09/216, 021

ICR FILING DATE: December 22, 1998

ICR APPLICATION NUMBER: 09/254,311

ICR FILING DATE: March 3, 1999

ICR FILING DATE: March 3, 1999

ICR FILING DATE: June 22, 1999

ICR APPLICATION NUMBER: PCT/US99/1252

ICR FILING DATE: June 27, 1999

ICR APPLICATION NUMBER: PCT/US99/21090

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OR FILING DATE: December 16, 1997
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OR FILING DATE: December 17, 1997
OR APPLICATION NUMBER: 60/068,017
OR FILING DATE: December 18, 1997
OR APPLICATION NUMBER: 60/070,440
OR FILING DATE: JANUARY 5, 1998
OR APPLICATION NUMBER: 60/074,086
OR FILING DATE: February 9, 1998
OR APPLICATION NUMBER: 60/074,099
OR FILING DATE: February 9, 1998
OR APPLICATION NUMBER: 60/074,099
OR APPLICATION NUMBER: 60/075,945
OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 60/112,850
OR APPLICATION NUMBER: 60/113,296
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FILING DATE: No. US20020127643A1ember 30,
APPLICATION NUMBER: PCT/US99/28313
FILING DATE: No. US20020127643A1ember 30,
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
FILING DATE: December 1, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
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FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
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APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16, 1999
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       Score 2263;
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Sequence 61, Application US/09945587 Patent No. US20020127643A1

APPLICANT: Baker, I APPLICANT: Botstej APPLICANT: Eaton,I APPLICANT: Ferrary

Botstein, David

Kevin

APPLICANT: APPLICANT:

Gerritsen, Mary Goddard, Audrey

Ferrara, Napoleone Filvaroff, Ellen

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Godowski,Paul Grimaldi,Christopher Gurney,Austin Hillan,Kenneth

APPLICANT:

APPLICANT:

Roy, Margaret Tumas, Daniel Wood, William

Napier, mary

Kljavin, Ivar

APPLICANT:

GENERAL

INFORMATION

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APPLICANT: Napie:/mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILTE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/945,015
CURRENT APPLICATION NUMBER: 001-09-26
PRIOR APPLICATION NUMBER: 00/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR APPLICATION NUMBER: 60/069335
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PRIOR APPLICATION NUMBER: 60/06937
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Hillan, Kenneth
Kljavin, Ivar
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Filvaroff, Ellen
Gerritsen, Mary
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                                      ; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo S
US-09-945-015-61
                                                                                                                                  NUMBER OF SEQ
SEQ ID NO 61
Query Match
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IOR APPLICATION NUMBER: 60/075,945
IOR APPLICATION NUMBER: 60/075,945
IOR FILING DATE: February 9, 1998
IOR APPLICATION NUMBER: 60/115,945
IOR FILING DATE: Hebernary 25, 1998
IOR APPLICATION NUMBER: 60/113,296
IOR FILING DATE: December 16, 1998
IOR APPLICATION NUMBER: 60/146,226
IOR FILING DATE: December 12, 1998
IOR APPLICATION NUMBER: 60/146,229
IOR FILING DATE: September 16, 1998
IOR APPLICATION NUMBER: PCT/US98/19330
IOR FILING DATE: December 1, 1998
IOR APPLICATION NUMBER: PCT/US98/25108
IOR FILING DATE: December 16, 1998
IOR APPLICATION NUMBER: 09/218,517
IOR FILING DATE: December 16, 1998
IOR APPLICATION NUMBER: 09/218,517
IOR FILING DATE: December 12, 1998
IOR APPLICATION NUMBER: 09/254,311
IOR APPLICATION NUMBER: 09/254,311
IOR FILING DATE: March 3, 1999
IOR APPLICATION NUMBER: PCT/US99/12552
IOR FILING DATE: June 22, 1999
IOR APPLICATION NUMBER: PCT/US99/12552
IOR FILING DATE: September 15, 1999
IOR APPLICATION NUMBER: PCT/US99/28409
IOR APPLICATION NUMBER: PCT/US99/28409
IOR FILING DATE: NO. US20020122768ALember 30
IOR ADDITICATION NUMBER: PCT/US99/28409
IOR FILING DATE: NO. US20020122768ALember 30
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OR APPLICATION NUMBER: 60/069,696
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,694
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,709
OR FILING DATE: December 16, 1997
OR APPLICATION NUMBER: 60/069,870
OR FILING DATE: December 17, 1997
OR APPLICATION NUMBER: 60/069,870
OR APPLICATION NUMBER: 60/069,870
OR APPLICATION NUMBER: 60/069,870
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APPLICATION NUMBER: PCT/US00/03565
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FILING DATE: No. US20020132768A1ember 30,
APPLICATION NUMBER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
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FILING DATE: January 5, 1998
APPLICATION NUMBER: 1998
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APPLICATION NUMBER: 60/068,
FILING DATE: December 18, 1
                                                                                                                                                                                                                                                                                            FILING DATE: March 30, 2000
APPLICATION NUMBER: PCT/US00/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US00/08439
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: February 22, 2000
APPLICATION NUMBER: PCT/US00/05841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
                                                                                                                                                                                                                                                 FILING DATE: July 28, 2000
APPLICATION NUMBER: PCT/US00/32678
  99.1%;
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  Score 2263;
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  Length 440;
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Best Lo Matches	Best Local Similarity 99.5%; Pred. No. 3.8e-175; Matches 440; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
δλ	1 MASVVLPSGSQCAAAAAAAAPPGLRIRLILLILFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
Вb	1 MASVVLPSGSQCAAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA 58
Ωγ	61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
망	59 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 118
γQ	121 RYFCQLYTDDDQESYTTITVLVPPRNLMIDIQXDTAVEGEEIEVNCTAMASKPATTIRWF 180
Вb	119 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQXDTAVEGBEIEVNCTAMASKPATTIRWF 178
Qγ	181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
Db .	179 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 238
δ	241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
Вb	239 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 298
γŞ	301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDDPTTIPPPTTTTTTTTTTTTTTTTILTIITD 360
Вb	299 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTILTIITD 358
Ş	361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
Db	359 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 418
γ	421 DTAIINAEGGONNSEEKKEYFI 442
Вb	419 DTAIINAEGGONNSEKKEYFI 440
Search co	completed: July 7, 2004, 06:39:08

Search completed: July 7, 2004, 06:39:08 Job time: 636.619 secs

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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

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Gapop 10.0 ,
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US-08-659-984A-5
US-08-659-984A-1
US-08-659-984A-1
US-08-659-984A-1
US-09-778-510-6
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US-09-733-368-4
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US-08-622-725-36
US-08-389-459A-17
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SEQ ID NO 20
LENGTH: 442
TYPE: PRT
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	Sequence 404, App Sequence 531, App Sequence 46, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 41, Appli Sequence 42, Appli Sequence 43, Appli Sequence 4, Appli Sequence 34, Appli Sequence 334, App Sequence 334, App Sequence 334, App Sequence 334, App Sequence 334, App Sequence 334, App Sequence 334, App Sequence 334, App Sequence 334, App Sequence 334, App Sequence 60, Appli Sequence 60, Appli	

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; ORGANISM: Homo sapien US-09-778-510-20
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Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHE
APPLICANT: TREEVES, Roger
APPLICANT: VOSHINGE, Muramaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
FILE REFERENCE: JHU1770-1
CURRENT APPLICATION UNMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 1
LENGTH: 442
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US-09-930-803-1
Sequence 61, Application U
, Patent No. 6642360
, GENERAL INFORMATION:
, APPLICANT: Baker, Kevin
, APPLICANT: Botstein, Davi
                                                             RESULT 3
US-09-866-028-61
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 Baker, Kevin
Botstein,David
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Pred. No. 6.6e-192;
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   GENERAL INFORMATION:
APPLICANT:
Baum, Peter
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/778,510
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Best Local Similarity
Matches 440; Conserv
                                                               Sequence 22, Application Patent No. 6512095
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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                              Molecules Designated
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pred. No. 3.7e-190;
0; Mismatches 0;
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Sequence 5, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESSEDING ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE:

PRIOR APPLICATION NUMBER:

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PRIOR FILING DATE:

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS:

SOFTWARE:

PATENTIN Ver. 2.0

SEQ ID NO 22

LENGTH: 423
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US-08-659-984A-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                STATE: C
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ilarity 98.8%;
Conservative 1
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PCT/US99/17906
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Pred. No. 6.1e-182;
1; Mismatches 4;
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MESULT 6 US-08-660-531-5 ; Sequence 5, Application US/08660531 ; Patent No. 6221645

GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase

NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:

ADDRESSEE:

Townsend and

Townsend

and Crew LLP

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Best Local :
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APPLICATION NUMBER: US/08/659,98

FILING DATE: 07-UN-1996

CLASSIFICATION: 436

PRIOR APPLICATION DATA;

APPLICATION NUMBER: US 08/485,15

FILING DATE: 07-UN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Heslin, James M.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 15270-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-236-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
 430
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                                                                                                                                               ELTCEAIGKPOPYMYTWVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGK
                                              P----DHALIGGIVAVVVFVTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINA
                                                                                             SSAEYVLIVHDVPNTLLPTTIIPSLTTATVTTTVAITTSPTTSATTSSIRDPNALAGONG
                                                                                                                     amino acids
             EGGQNNSEEKKEYFI
                                                                    SIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINA
                                                                                                                                                                                                LDFRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPFPQEGQPL
                                                                                                                                                                                                                        QISGFSSPVMEGDLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSST
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Pred. No. 8.3e-71;
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Best Local S
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INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-236-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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LENGTH: 444 amino acid
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                    322 AHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIIT-------DSRAGEEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 LMLKVHKEDDGVFVICQVEHPAVTGNLQ-TQRYLEVQYKFQVHIQMTYFLQGLTREGDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWS---DMYTVTSQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tch 39.5%; Score 902; DB 3; Length 444; al Similarity 44.6%; Pred. No. 8.3e-71; 194; Conservative 74; Mismatches 137; Indels
1, Application US/08659984A
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                                                                                                                                                                                                                      SIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINA
                                                                                                                                                                                             P----DHALIGGIVAVVVFVTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTÄIINÄ
                                                                                                                                                                                                                                                                                                                                                                                                                                               LDFRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPFPQEGQPL
                                                                                                           EGSQVNAEEKKEYFI 444
                                                                                                                                                  EGGONNSEEKKEYFI 442
                                                                                                                                                                                                                                                                               SSAEYVLIVHDVPNTLLPTTIIPSLTTATVTTTVAITTSPTTSATTSSIRDPNALAGQNG
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; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-659-984A-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15:
TELECONMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING_DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compactante
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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384 VVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
                                                                        307 LPTTIIPSLTTATVTTTVAITTSPTTSATTSSIRDPNALAGQNGP----DHALIGGIVAV
                                                                                                                   247 WTKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCEATNTIGQSSAEYVLIVHDVPNTL
                                                                                                                                                                                                                                                           190 RVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPFPQEGQPLILTCESKGKPLPEPVL
                                                                                                                                                                                                                                                                                                                                                       130 LTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSTLDFRVDRSDDGVAVIC
                                                                                                                                                                                                                                                                                                                                                                                                  164 VNCTAMASKPATTIRWFKGNTELKGKSEVEEWS---DMYTVTSQLMLKVHKEDDGVPVIC
                                                                                                                                                                                                             280 WYRYDDEM--POHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTI 337
                                                                                                                                                                                                                                                                                                        221 QVBHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 SSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 GQFPLTQNVTVVEGGTAILTCRVDQNDNTSLQWSNPAQQTLYFDJXXALRDNRIELVRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 GONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFS 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 WHELSISVSDVSLSDEGQYTCSLFTMPVKTSKAYLTVLGVPEKPQISGFSSPVMEGDLMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 39.2%; Score 895.5; DB 2; Similarity 45.1%; Pred. No. 2.9e-70; 89; Conservative 73; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 27;
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306

246

129 220

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363 VVFVTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINAEGSQVNAEEKKEYFI 421

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US-08-660-531-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.2%; Score 895.5; DB 3; Length 421; Best Local Similarity 45.1%; Pred. No. 2.9e-70; Matches 189; Conservative 73; Mismatches 130; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION UNDER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chrysler, Susanna M.S. APPLICANT: Sinha, Sukanto APPLICANT: Keim, Pamela S. APPLICANT: Anderson, John P. TITLE OF INVENTION: Beta-Secretase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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STATE: California
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                         247 WTKDGGELPDPDRMVVSGRELNILPLNKTDNGTYRCEATNTIGQSSAEYVLIVHDVPNTL 306
                                                           280 WYRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTI 337
                                                                                                                                                                                                                                     130 LTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSTLDFRVDRSDDGVAVIC 189
                                                                                                                                                                                                                                                                                                                                                                     104 SSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQXDTAVEGEEIE 163
                                                                                                                                                                            221 QVEHPAVTGNIQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVT 279
                                                                                                                                                                                                                                                                                     164 VNCTAMASKPATTIRWFKGNTELKGKSEVEEWS---DMYTVTSQLMLKVHKEDDGVPVIC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                            10 GQFPLTQNVTVVEGGTAILTCRVDQNDNTSLQWSNPAQQTLYFDDKKALRDNRIELVRAS 69
                                                                                                                                                                                                                                                                                                                                     70 WHELSISVSDVSLSDEGQYTCSLFTMPVKTSKAYLTVLGVPEKPQISGFSSPVMEGDLMQ 129
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                         US-09-778-510-6

; Sequence 6, Application US/09778510

; Patent No. 6512095
GENERAL INFORMATION:
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SOUT 9 50-4 Sequence 4, Application US/09778510 Sequence 4, Application US/09778510 Sequence 4, Application US/09778510 Sequence 4, Application US/09778510 Sequence 4, Application US/09778510 Sequence 4, Application US/09778510 Sequence 4, Application US/09778510 Sequence 4, Application US/09778510 Sextent No. 6512095 Sextent No. 6512095 Sextent No. 6512095 Sextent No. 1294-US CURRENT FILIKO DATE: 201-02-07 Sextent Application Number: DCTUS99/17906 Sextent No. 1298-08-05 Sextent Number: 22-00-05-663 Sextent Number: 1298-08-05 Sextent Number: 1298-08-05 Sextent Number: 1298-08-05 Sextent Number: 1298-08-07 Number of Sextent Ver. 2.0 LENGTH: 398 TYPE: PRT ORGANIAM Mus muscullus -09-778-510-4 LENGTH: 398 Sextentive 74; Mismatches 137; Indels 57; Gaps 16 AAAAAPPGLERIELLLLESAAALIPTGBGQNLFTKDVTVIBGEVATICCQVNKSD Sextentive 172; Conservative 74; Mismatches 137; Indels 57; Gaps 16 AAAAAPPGLERIELLLLLESAAALIPTGBGQNLFTKDVTVIBGEVATICCQVNKSD Sextentive 172; Conservative 74; Mismatches 137; Indels 57; Gaps 16 AAAAAPPGLERIELLLLLESAAALIPTGBGQNLFTKDVTVIBGEVATICCQVNKSD Sextentive 172; Conservative 74; Mismatches 137; Indels 57; Gaps 16 AAAAAPPGLERIELLLLLESAAALIPTGBGQNLFTKDVTVIBGEVATICCQVNKSD Sextentive 172; Conservative 74; Mismatches 137; Indels 57; Gaps 17 DSVIQLENPARGTIYFEDFRELKDSRFQLLNFSSEELKVSLTNVSISDEGRYFCQLYTDF Sextentive 172; Conservative 74; Mismatches 137; Indels 57; Gaps 18 APASP
510-4 FERENCE SEE SEE SEE SEE SEE SEE SEE SEE SEE S
510-4 NT: OR SEPTION FEITH OR SEPTION F
510-4 510-4 510-4 510-4 510-4 510-4 510 510 510 510 113 11
510-4 NOTE:
510-4 A, Application US/0977 10. 6512095 INFORMATION: PERENCE: PINVENTION: PERLICATION UNMBER: PEPLICATION UNMBER: VEPLICATION UNMBER: VILING DATE: 2001-02- PEPLICATION UNMBER: VILING DATE: 1999-08 PEPLICATION UNMBER: 1998-08 PER US PATENTIN Ver. 2. 10 4 10 398 PRT SM: Mus musculus 510-4 172; Conservative 7 16 AAAAAAPPGLERLILLLLES 1 3 APAASPVPLILLL-
510-4 14, Application US/09778510 10. 6512095 INFERMATION: DIFFERMATION: FERRINCE: 2844-US APPLICATION NUMBER: US/09/778,510 FILING DATE: 2001-02-07 FPLICATION NUMBER: PCT/US99/17906 FILING DATE: 1999-08-05 ILING DATE: 1999-08-05 ILING DATE: 1998-08-07 OF SEC DATE: 1998-08-07 OF SEC DATE: 22 E: PALCATION NUMBER: 22 DF SEC DATE: 2.0 04 1: 398 9RT SM: Mus musculus

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US-09-907-794A-84
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; ORGANISM: Homo sapien
US-09-778-510-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
SOFTWARE:
SEQ ID NO 6
                                                                                                                                                                                                                                                      Sequence 84, Application US
Patent No. 6635468
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                            APPLICANT:
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PRIOR APPLICATION NUMBER: 1998-08-0
PRIOR FILING DATE: 1998-08-0
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
NUMBER OF SEQ ID NOS: 22
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CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
CURRENT FILING DATE: 2001-02-07
                                                                                                                       APPLICANT:
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                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                  389 GGDDKKEYFI 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 CEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 ---HPREGQKLLLHCEGRGNPVPQQYLWEK-EGSVPPLKWTQESALIFPFLNKSDSGTYG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 LQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 PNGKTFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 SD--MYTYTSQLMLKVHKEDDGVPVICQVEHPAVIG-NLQTQRYLEVQYKPQVHIQMIYP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 LVTVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQED 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 TITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGK-SEVEEW 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 LNPNRQTIYERDERPLKDSREQLLNESSSELKVSLTNVSISDEGRYECQLYTDPPQESYT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 PGLRLRLLLLFSAAALIPTG-----DGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 PAASILLLLLIF-ACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW 62
                                                                                                                                 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
                                    Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQN 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTATSNMGSYKAYYTLNVNDPS---PVPSSSSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -HATIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDDAPDADTAIINAEGGQS
                                                                                                                                                                                                                                                                                                                    Application US/09907794A
                                                                                                                  Fong,
Godowski, Paul J.
Grimaldi, Christopher J.
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                                                                                                                     Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.4%; SCOLE ... 1.4e-56; 38.6%; Pred. No. 1.4e-56; Indels tive 73; Mismatches 147; Indels
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1999-08-05
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-84
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR TILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
                                                                                                                                                                                                                                                              Query Match 32.4%; Score 739; DB 4; Length 398; Best Local Similarity 38.6%; Pred. No. 1.4e-56; Matches 166; Conservative 73; Mismatches 147; Indels
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PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
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CURRENT FILING DATE: 2001-07-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFFLICARY: WOOD, WILLIAM, 1.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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OR APPLICATION NUMBER: PCT/US99/20944
OR FILING DATE: 1999-09-13
OR APPLICATION NUMBER: PCT/US99/21090
OR FILING DATE: 1999-09-15
OR APPLICATION NUMBER: PCT/US99/21547
OR APPLICATION NUMBER: PCT/US99/23089
OR APPLICATION NUMBER: PCT/US99/23089
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FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/30911
FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
123 LVTVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQED
                                      137 TITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGK-SEVEEW
                                                                                      63 SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSISISNVALADEGEYTCSIFTMPVRTAKS
                                                                                                                          77 INPURQTIYERDERPLKDSRFQLLNESSSELKVSLTNVSISDEGRYFCQLYTDPPQESYT
                                                                                                                                                                                                                     22 PGLRIRILLIESAAALIPTG-----DGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQL
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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art, Timothy A.
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                                                                                                                                                                                                                                                                   Indels 44;
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20594
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US-09-905-125A-84
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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APPLICANT:
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
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                                                                                APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/20944
FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
                    APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Godowski, Paul J.
Grimaldi, Christopher
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                  NUMBER: PCT/US99/23089
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argaret Ann
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Sequence 84, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Desnoyers, Luc
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-00
PRIOR PILING DATE: 1999-12-00
PRIOR PILING DATE: 1999-12-00
PRIOR PILING DATE: 1999-12-00
PRIOR PILING DATE: 1999-12-00
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF 580 ID NOS: 423
SEQ ID NO 84
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US-09-902-775A-84
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TYPE: PRT
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OR APPLICATION NUMBER: PCT/US99/28214
OR FILING DATE: 1999-11-29
OR APPLICATION NUMBER: PCT/US99/28313
OR APPLICATION NUMBER: PCT/US99/28313
OR APPLICATION NUMBER: PCT/US99/28564
OR APPLICATION NUMBER: PCT/US99/28564
OR APPLICAN DATE: 1999-12-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 PGLRĻRĻĻĻĻĻESAMALIPTG-----DGQNLETKDVTVIEGEVATISCQVNKSDPSVIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PAASLLLLLLLF-ACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---HPREGOKLILHCEGRGNEVPQQYLWEK-EGSVPPLKWTQESALIFPFLNKSDSGTYG
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Pred. No. 1.4e-
73; Mismatches
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Length 398; Indels

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PRIOR FILING DATE: 1999-07-07
PRIOR PELICATION NUMBER: US 60/145,698
PRIOR RELING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR RILING DATE: 1999-09-13
PRIOR RELING DATE: 1999-09-13
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TILE REFERENCE: 10466-14
TIDEDEFORM TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PRO
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION UNMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
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OR APPLICATION NUMBER: PCT/US99/30095
OR FILING DATE: 1999-12-16
OR APPLICATION NUMBER: PCT/US99/30911
OR FILING DATE: 1999-12-20
OR APPLICATION NUMBER: PCT/US99/30999
OR APPLICATION NUMBER: PCT/US99/30999
OR FILING DATE: 1999-12-20
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APPLICATION NUMBER: PCT/US99/28565
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FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
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                                                                                                                                                                                                                166;
77 LNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYT 136
                                                                                                                                      22 PGLRLRLLLLLFSAAALIPTG-----DGQNLFTKDVTVIEGEVATISÇQVNKSDD$VIQL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                        398
                                                                   4 PAASILLLLLIF-ACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW 62
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Godowski, Paul J.
Grimaldi, Christopher J.
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                     32.4%; Score 739; DB 4; Length 398; 38.6%; Pred. No. 1.4e-56; ative 73; Mismatches 147; Indels
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; SOFTWARE: PatentIn v
SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
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US-09-778-510-2
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Best Local :
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GENERAL INFORMATION:
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PRIOR FELICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1996-08-07
NUMBER OF SEQ ID NOS: 22
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CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
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                                                                                                  183 TLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFTVSSSVTFQVTREDDGASIV
                                                                                                                                                                                                       123 TPHELSISISNVALADEGEYTCSIFTMPVRTAKSLVTVLGIPQKPIITGYKSSLREKDTA 182
                                                                                                                                                                                                                                   103 SSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEI 162
                                               220 CQVEHPAVTG-NLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMV 278
                                                                                                                                                    163 EVNCTAMASKPATTIRWFKGNTELKGK-SEVEEWSD--MYTVTSQLMLKVHKEDDGVPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169; Conservative
                                                                                                                                                                                                                                                                                                               63 QDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWSNPAQQTLYFGEKRALRDNRIQLVTS
                                                                                                                                                                                                                                                                                                                                                              48 ----FTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNF 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 PGLRIRLLLLESAAALIPTG-----DG----QNL--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 31.6%; Score 722; DB 4; J
Similarity 36.4%; Pred. No. 4.9e-55;
69; Conservative 74; Mismatches 143;
CSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPP---HPREGQKLLLHCEGRGNPVPQQY 299
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GENERAL INFORMATION:
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
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CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
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2R FILLING DATE: 1997-06-06
2R APPLICATION NUMBER: 60/048,972
2R FILLING DATE: 1997-06-06
2R APPLICATION NUMBER: 60/048,916
2R FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,019
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
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APPLICATION NUMBER: 60/048,900
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APPLICATION NUMBER: 60/049,375
FILING DATE: 1997-06-06
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LENGTH: 227
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ER APPLICATION NUMBER: 60/048,875
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FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,974
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APPLICATION NUMBER: 60/048,897
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K-EGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKAYYTLNVND
                                                              NHESLKGADRSTSQRIEVLYTPTAMIRPDPP---HPREGQKLLLHCEGRGNPVPQQYLWE
                             RVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYD 332
                                                                                           EHPAVIG-NIQTORYLEVOYKPQVHIQMTYPLOGLTREGDALELTCEAIGKPOPVMVTWV
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                                                                                             PRR2 alpha - human opicid-binding pro opicid-binding cel surface glycoprote adhesion molecule
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neural cell adhesi
50K glycoprotein p
PRR2 alpha - human
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elastic titin - hu
connectin/titin -
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                        adhesion mole
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A;Molecule type: mRNA A;Residues: 1-407 <OTT> A;Cross-references: EMBL:AL050071

Experimental source: fetal kidney; clone DKFZp566B0846

R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08732

S

hypothetical protein DKFZp566B0846.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08732

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ALIGNMENTS

밁 Ś 멂 밁 Š Ş 맑 Ś 밁 Ś A;Note: Query Match Best Local S Matches 85 DKFZp566B0846.1 376 286 233 325 173 273 115 102 GRYFCQLYTDP--PQESYTTITVLYPPRNLMIDIQKDTAVEG--EEIEVNCTAMASKPAT 157 158 TIRWFKGNKELKGKSEVEEWSDMY-----TVTSQLMLKVHKEDDGVPVICQVEHPAVTGN 213 LQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQH 61 85; 2 GKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLIDGGNETVAAICIAATGKPVA Similarity LLASDNTLHEVHPLTFNYSGYYICKVINSLGQRSDQKVIYISDPPTTTTLQPTIQWHPST YRRRTFRGDYFAKN 300 -----ILGRYFARH 384 TTTTTTTT-----TTTILTIITDSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLI- 375 AVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPP--TTIPP-----PTT IRYSFILDIQYAPEVSVTGYDGNWFVGRKG--VNLKCNADANPPPFKSVWSRLDGQWPDG HIDW-EGD-----LGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKD ADIEDLATEPKKLPFPLSTLATI-----KDDTIATIIASVVGGALFIVLVSVLAGIFC Conservative 12.3%; 58; Score 270; DB 2; Pred. No. 1.1e-11; Mismatches 124; Length 407; Indels 48; Gaps 172 324 60 272 114 212 232

hypothetical protein F15G9.4a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T20992; T24733

RESULT T20992

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hemicentin precursor - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 18-Feb-2000
C,Accession: T43290; T20993; T24734
R,Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A,Description: Hemicentin is required for hemidesmosome mediated cell adhes.
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submitted to the EMBL Data Library,
A;Reference number: Z19929
A;Accession: T24733
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R;Sulston, J.
submitted to the EMBL Data
A;Reference number: Z19355
A;Accession: T20993
                                                      A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>
A;Cross-references: EMBL
R;Sulston, J
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A; Map position: X
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A; Residues: 1-5175 <WI2>
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                                                                                                               A;Accession: T43290
A;Status: preliminary; translated from A;Molecule type: mRNA
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Best Local S
Matches 87
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;Residues: 1-5175 <WIL>
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87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VTAIKGGALPFKCPID--DDK-----NFKGQIIWLRNYQPIDLEAEDARITRL---SNDR
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                                                                                EMBL:AF074901;
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                                          Library,
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Pred. No. 1.1e-09;
55; Mismatches 130;
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                                                                                PIDN: AAC26792.1
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poliovirus receptor homolog precursor - mouse C;Species: Mus musculus domesticus (western European house mot C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_chang C;Accession: A38211
R;Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A;Title: Molecular cloning and expression of a murine homolog A;Reference number: A38211; MUID:92219365; PMID:1560525
A;Accession: A38211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R)Kershaw, J.
submitted to the EMBL Data Library,
*-Pafarence number: Z19929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5198 <WIL>
A;Cross-reference: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028;
A;Experimental source: clone F15G9
A;Cross-references: GBLM80206; NID:g199785; PIDN:AAA39734.1;
C;Gupertamily: poliovirus receptor; immunoglobulin homology
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-467/Product: poliovirus receptor homolog #status predict
F;26-354/Domain: extracellular #status predicted <EXT>F;47-133/Domain: immunoglobulin homology <IMM2>F;47-332/Domain: immunoglobulin homology <IMM2>F;357-374/Domain: transmembrane #status predicted <TWN>F;355-374/Domain: transmembrane #status predicted <TWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Experimental source: clone T09B9 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-5198 <WI2>
A;Cross-references: EMBL:Z47070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A; Accession: T24734
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                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-467 < MOR>
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87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 261.5; DB 2; Pred. No. 1.1e-09;
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(western European house mouse)
sion 30-Jun-1993 #text_change ?
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A;Gene: GDB:PVRR1
A;Cross-references: GDB:583951
A;A;Cross-references: GDB:583951
A;A;Ag position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-518/Product: poliovirus receptor-related protein #status processed for transmembrane for the protein for the protein for the protein for the process of the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for the protein for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 155, 261-265, 1995
A; Title: Complementary DNA characterization
A; Reference number: JC4024; MUID:95237621; 1
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C;Genetics:
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A; Residues: 1-518 < LOP>
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F;54-131,174-229,274-320/Disulfide bonds: #status predicted
F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #
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Matches 101;
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                                                                                                                                   Query Match
Best Local
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                                                                                                                                   Similarity
            VAIYNPSMGVSVLAPYR---
                                                      IQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPP--
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larity 25.1%;
Conservative 5:
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21.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID: 9732795;
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Pred. No. 6e-10
72; Mismatches
                                                                                                       Score 244; DB 2
Pred. No. 1e-09;
9; Mismatches 1
          -ERVEFLRPSFTDGTIRLSRLELEDEGVYICEFATFPTGN
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No. 6e-10;
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                                                                                                                                                   DB 2; Length 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN: CAA53980.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A. J. Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved A;Reference number: A53437; MUID:94179228; PMID:8132569
A;Accession: A53437
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A;Molecule type: mRNA
A;Residues: 1-530 <AOK>
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G;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
G;Accession: A53437
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FPASAVAQGSQLLVHSVDRMVNTTFICTATNAVGTGRAEQVILVRESPST-
                                              MPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTT
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                                                                                               FEEPILLPVTLSVRYPPEVSIS-GYDDNWYLGRSEAI-LTCDVRSNPEPTDYDWSTTSGV
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Pred. No. 1.2e-09;
1; Mismatches 162;
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A;Cross-references: GB:S79172; NID:g1042204; PID:g1042205
C;Genetics:
A;Gene: PRR2delta
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus A;Reference number: I53960; MUID:95347610; PMID:7622062
                                                     RESULT
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A;Residues: 1-538 <RES>
A;Cross-references: GB:S79172; NID:g1042204; PID:g1042205
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence revision 29-May-1998
C;Accession: I68093
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neural cell adhesion molecule 1 - African N;Alternate names: N-CAM 1 C;Species: Xenopus laevis (African clawed C;Date: 19-May-1998 #sequence_revision 29-
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                              TWVRVDDEMPQHAVLSGENLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIP
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                                                                                                                                                                                                                                                                                                                                              ICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPGLYISLVTWQRPDAPANHONV--AAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTE
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                                                                                                                                                                                                                                           PPTTTTTTTTTTTTLITITDSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.9%; Score 238.5; DB 2 ilarity 22.8%; Pred. No. 2.6e-09; Conservative 63; Mismatches 196
                                                                                                           440
                                                                                                                                    423
                                                                                                                                                              -LQGAEEDEDLEGPPSYKPPTPKAKLEAQEMPSQLFTLGASEHSPLKTP 438
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                                                                                                                                                                                                                  29-May-1998 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --IİĞĞIIAAII 361
                                          clawed
                                                                                                                                                                                        ---TAIINAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196;
                                        frog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---QLLNFSSS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       538;
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                                                                                                                                                                                        GGONNSEEKKE
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Best Local S
Matches 89
                                                                                               Query Match
Best Local S
Matches 107
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C;Accession: JE0099

R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of sed-form neural cell adhesion molecules
A;Reference number: JE0099; MUID:98204770; PMID:9535795
A;Accession: JE0099.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  poliovirus receptor (clone AGM-alpha-1) - green monkey c;Species: Cercopithecus aethiops (green monkey, grivet) c;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_C;Accession: A44194 #S;Roike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; J. Virol. 66, 7059-7066, 1992 A;Title: A second gene for the African green monkey polion;Reference number: A44194; MUID:93059651; PMID:1331508 A;Accession: A44194 #Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: This protein mediates and regulates various cell-cell interactions through bo C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu F;413-475/Domain: immunoglobulin homology <IMM> F;512-589/Domain: fibronectin type III repeat homology <3FR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1;
A;Experimental source: heart
A;Experimental source:
                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:S48777
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: transmembrane protein
F;259-314/Domain: immunoglobulin homology <INM>
                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-417 < KOI >
57 QLINDUR-----QTIYFRDFRPLKDSRFQLINFSSSSELKVSLTUVS------ISDEGRY
                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNFSSSELKVSLTNYSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFILVQADTPSS---PAIRKVEPYSSTVMIVFDEPDSTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEITLICEA-SGDPIPSITWRTAVRNISSEATTLDGHIVVKEHIRM----SALTLKDIQY 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBIEVNCTAMASKPATTIRWFKGNKE-----LKGKSEVEEWSDMYTVTSQLMLKVHKE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDIQVIVNVPPTIQARQLRVNATAKMAESVVLSCDADGFPDPEISWLKKGEPIEDGE-EK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDVTVIEGEVATISC---QVN---KSDDSVIQLLN----PNRQTIYFRDFRPLKDSRFQL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR-AAVTWFRDGQLLPSSNFSNIKIYSGPTSSSLEVNPDSENDFGNYNCTAINTIGHEFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR----GPVVVYTWEGNPVNITCEVFAH 425
                                                                                                                                          AAPPGLRLRLLLLLSAAALIPTGDGQNLFTKDVTV--IEGEVATISC--QVNKSDDSVI
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Conservative 61
                                                                                                                                                                                                     Conservative
                                                                                        LLLTLLELSWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHV
                                                                                                                                                                                                                         10.8%;
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Pred. No. 4.2e-09;
51; Mismatches 148
                                                                                                                                                                                               Score 237; DB 2; L
Pred. No. 2.4e-09;
8; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  en monkey poliovirus receptor
PMID:1331508
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poliovirus receptor (clone AGM-delta-1) - green monkey
()Species: Cercopithecus aethiops (green monkey, grivet)
()Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2
()Accession: B44194
R;Koike, S.; Ise, I; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Status: preliminary
A;Status: preliminary
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C:Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-392 < KOI>
                                                                                    277
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                                                                                                                             VNLTVYYPPEVSIS-GYDNNWYLSQNEA-TLTCDARSNPEPTGYNWSTTMGPLPPFAVAQ
                                                                                                                                                                              RYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLS 276
                                                                                                                                                                                                                                  W---HSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTCKVEHESFEKPQLLT
                                                                                                                                                                                                                                                                                   WEKGNKELKGKSEVEE----WSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQ
                                                                                                                                                                                                                                                                                                                                                                                     FCQLYTDPPQESYTT---ITVLVPPRNLMIDIQKDTAVEGEEIEV-NCTAMASKPATTIR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                         SQLTWSRHGESGSMAVFHQTQGPNYSEPKRLEFVAARLGTELRDASLRMFGLRVEDEGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AWPP-----LLLTLLELSWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHV
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                                GAQLLIRPVDKPINTTFICNVTNALGARQAELTVQVKEGPPSEPS--
                                                                            GPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTI
                                                                                                                                                                                                                                                                                                                                       TC-LFVTFPQGSRSVDIWLRVLAKPQN-TAEVQK-VQLTGKPVPVARCVSTGGRPPAHIT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLLNPNR-----QTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS-----ISDEGRY 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W----HSDLGGMPNTSQAPGFLSGTVTVTSLWILVPSSQVDGKSVTCKVEHESFEKPQLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQLTWSRHGESGSMAVFHQTQGPNYSEPKRLEFVAARLGTELRDASLRMFGLRVEDEGNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 234.5;
Pred. No. 3.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.4e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <IF;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status predicted <EXT>
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <ITMM1>
F;129-188/Domain: immunoglobulin homology <ITMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;25-284/Domain: immunoglobulin homology <ITMM3>
F;317-381/Domain: immunoglobulin homology <ITMM5>
F;117-49/Domain: immunoglobulin homology <ITMM5>
F;618-679/Domain: fibronectin type III repeat homology <FN3A>
F;618-679/Domain: transmembrane #status predicted <ITM5>
F;706-723/Domain: intracellular #status predicted <ITM5>
F;706-723/Domain: intracellular #status predicted <ITM5>
F;71-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;319,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 1-1088 <KRI>
A;Residues: 1-1088 <KRI>
A;Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610
A;Note: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with and
C;Comment: Several forms of NCAM are produced by alternative splicing.
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C; Superfamil
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Nucleic Acids Res. 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression
A;Reference number: S09600; MUID:90098871; PMID:2481269
A;Accession: S09600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neural cell adhesion molecule long domain form precursor - Afric N;Alternate names: NCAM-180 N;Contains: neural cell adhesion molecule, short domain form (NCC;Species: Xenopus laevis (African clawed frog) C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change C;Accession: S09600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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  EFILVOADTPSS---PAIRKVEPYSSTVMIVFDEPDSTGG
                                              DYMLYVYDPPTTIPPPTTTTTTTTTTTLTITTDSRAG 346
                                                                                                                                                                                                                                               DDGVPVICQVEHPAVTGNLQTQRXLEVQXKPQVHIQMTXPLQGLTREGDAFELTCEAIGK
                                                                                                                                                                                                                                                                                                                                       EEIEVNCTAMASKPATTIRWFKGNKE-----LKGKSEVEEWSDMYTVTSQLMLKVHKE
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                                                                                                  PR-AAVTWFRDGQLLPSSNFSNIKIYSGPTSSSLEVNPDSENDFGNYNCTAINTIGHEFS
                                                                                                                                                     PQPVMVTWVRVDDEMPQH----AVLSGP---NLFINNLNKTDNGTYRCEASNIVGKAHS
                                                                                                                                                                                                 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR----GPVVVYTWEGNPVNITCEVFAH
                                                                                                                                                                                                                                                                                                      DEITLTCEA-SGDPIPSITWRTAVRNISSEATTLDGHIVVKEHIRM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG
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N,Alternate names: poliovirus receptor H2OB
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A;Map position: 19913.2-19913.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor;
F;1-20/jomain: signal sequence #status predicted <SIG-
F;21-392/product: poliovirus receptor delta #status predicted <MAT-
F;21-343/jomain: extracellular #status predicted <EXT-
F;42-125/jomain: immunoglobulin homology <IVM1-
F;42-125/jomain: immunoglobulin homology <IVM1-
F;42-125/jomain: immunoglobulin homology <IVM1-
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A;Residues: 1-66,'A',68-392 <MEN>
A;Cross-references: GB;M24406
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A; Title: Cellular receptor for poliovirus: A; Reference number: A90910; MUID:89168426;
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A;Note: 67-Ala was also found
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello,
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7:259-314/Domain: immunoglobulin homology <IMM2>
7:259-314/Domain: immunoglobulin homology <IMM3>
7:344-367/Domain: intransembrane #status predicted <IMN>
7:368-392/Domain: intracellular #status predicted <INT>
7:368-392/Domain: intracellular #status predicted <INT>
7:49-123,166-221,266-312/Disulfide bonds: #status predicted
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    RPVDKPINTTLICNVTNALGARQAELTVQVKE---
                                                                                                                                                                YPPEVSIS-GYDNNWYLGQNEA-TLTCDARSNPEPTGYNWSTTMGPLPPFAVAQGAQLLI 299
                                                                                                                                                                                                                                          YKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFVTFPQGSRSVDIWLRVLAKPQN-TAEVQK-VQLTGEPVPMARCVSTGGRPPAQITWHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLVALLVLSWPPPGTG-----DVVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             function of this receptor is unknown. Membrane-bound and soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 232.5; DB 1
Pred. No. 4.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     molecular cloning, PMID:2538245
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        -GPPSEHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
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C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; tran.
E;1-20/Domain: signal sequence #status predicted <SIG>
F;21-41//Product: poliovirus receptor alpha #status predicted <PVRA>
F;21-343/Domain: extracellular #status predicted <EXT>
F;21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRB>
F;42-125/Domain: immunoglobulin homology <IMM2>
F;45-125/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM3>
F;259-314/Domain: immunoglobulin homology <IMM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, EMBO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and A;Reference number: $12048; MUID:91006015; PMID:2170108
A;Accession: $12048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X64116; NID:g35809; PIDN:CAA45478.1; A;Note: 67-Ala was also found A;Note: the gamma form has 331-Gly and lacks residues 332-384 R;Mendelsohn, C, L; Wimmer, E.; Racaniello, V.R. Cell Ec occ occ 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-66, 'A', 68-417 < MEN>
A; Cross-references: GB: M29535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus:
A;Reference number: A90910; MUID:89168426;
A;Accession: A31496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-417 < KOI>
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C;Accession: S12048; A31496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poliovirus receptor splice form alpha precursor -
N;Alternate names: poliovirus receptor H2OA
N;Contains: poliovirus receptor beta
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Best Local
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223 YKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
                                                                             182
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                                                                                                                                                                                                                                                                                 TWTRHGESGSMAVFHQTQGPSYSESKRLEFVAARLGAELRNASLRMFGLRVEDEGNYTC-
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                                                                                DIGGMENTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHESFEKPQLLTVNLTVY
                                                                                                                           GNKELKGKSEVEEW-SDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 222
                                                                                                                                                                                                                                 LYTDPPQESYTT---ITVLVPPRNLMIDIQKDTAVEGEEIEV-NCTAMASKPATTIRWFK 163
                                                                                                                                                                                                                                                                                                                                 NPNR-----QTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS-----ISDEGRYFCQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLLLSAAALIFTGDGQNLFTKDVTV------IEGEVATISC--QVNKSDDSVIQLL
                                                                                                                                                                                                                                                                                                                                                                                       LILVALLVLSWPPPGTG
                                                                                                                                                                                LFVTFPOGSRSVDIWLRVLAKPON-TAEVOK-VQLTGEPVPMARCVSTGGRPPAQITWHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function of this receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%; Score 232.5; 25.3%; Pred. No. 5.1e tive 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    ---DVVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1e-09;
ches 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Asn)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71;
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                                                                                   241
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elastic titin - human (fragment)
()Species: Homo sapiens (man)
()Species: Homo sapiens (man)
()Clate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
()Accession: I38346
R.Labeit, S.; Kolmerer, B.
Science 270, 293-266, 1995
Science 270, 293-266, 1995
Science 17tins: giant proteins in charge of muscle ultrastructure and elast A;Reference number: A57430; MUID:96026330; PMID:7569978
A;Reference number: A57430; MUID:96026330; PMID:7569978
A;Accession: I38346
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-7962 <RES>
                                                                                                                                                                                                                                                                                                             RESULT 15
I38346
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 19-May-2000
C;Accession: I56551
R;Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer,
J. Neurosci. 15, 2141-2156, 1995
A;Title: Cloning of neurotrimin defines a new subfamily of differentially expressed
A;Reference number: I56551; MUID:95198094; PMID:7891157
A;Accession: I56551
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A;Molecule type: mRNA
A;Residues: 1-344 <RES>
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I56551
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C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precurso:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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Best Local S
Matches 85
    Cross-references: EMBL:X90569; NID:g1017426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     287
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85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVQVSPK--IVEISSDISINEGNNISLTCIA-TGRPEPTVTWRHISPKAVGFVSEDEYLE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                           KTDNGTYRCEASNIVGKAHSDYMLY 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IQGITREQSGEYECSASNDVAAPVVRRVN------VTVNYPPYIS-----EAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYTVTSQLMLKVH---KEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVLVPPRNLMIDIQKDTAV-EGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDNHPKTSRVHL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RQTI-YFRDFRFLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTD-PPQESYTTI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVVVSLRLLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCTI---DNRVTRVAWLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLLLISAAALIPTG----DGQNLFTK---DVTVIEGEVATISCQVNKSDDSVIQLLNPN
                                                                                                                                                                                                                                                                                                                                                                                                      EHDYGNYTCVASNKLGHTNASIMLF 311
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30 355 376 376 244 234 443

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE.

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

POLY-GLU.

POTENTIAL.
POLIOVIRUS RECEPTOR RELATED
EXTRACELLULAR (POTENTIAL).

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IAL N	adhesion; Immuno	T; SM004	terPro; IPR007110; terPro; IPR003596;	AF308632	send an er	modified and entities requ	European	SWISS-PROT	-!- SIMILARI	SUBUNIT: Into	FUNCTION: PROBAB ALPHAHERPESVIRUS CELLS:	s a functional alphaherpes rology 281:315-328(2001).	en G.H.;	JENCE FRO LINE=2117	Eukaryota; Metazoa; Cho Mammalia; Eutheria; Cet NCBI TaxID=9823;	SCrofa (iovirus r	16-0CT-2001	176; 176;			192.5			196.5	198	> 0 3
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SEQUENCE
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CARBOHYD
Lopez M., Eberie ...,
Dubreuil P.;
Dubreuil P.;
"cDNA characterization and chromosomal "cDNA characterization gene.";
                                                                                                                                                              PVR1 HUMAN STANDARD; PRT; 517 AA.

Q15223; O75465; Q9HBB6; Q9HBW2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Poliovirus receptor related protein 1 precursor (Herpes virus mediator C) (HyeC) (Nectin 1) (Herpesvirus Ig-like receptor) (
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                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                               SEQUENCE FROM N.A. MEDLINE=95237621;
                                                                                                                                          PVRL1 OR PRR1
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                                                                                                                                sapiens (Human)
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                                                                                                         ; Metazoa; Chordata;
Eutheria; Primates;
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PubMed=7721102;
F., Mattei M.-G.,
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24.5%;
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Pred. No. 2.2e
61; Mismatches
                                                                                                           Craniata; Vertebrata;
Catarrhini; Hominidae
                                                        Gabert
                                   localization
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NAT. Genet. 25:427-430(2000).
NAT. Genet. 25:427-430(2000).
-i- FUNCTION: PROBABLY INVOLVED IN
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Science
                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
MEDLINE=20392396; PubMed=10932188;
Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Geraghty R.J., Krummenacher C., Cohen
Spear P.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 155:261-265(1995).
[2]
SEQUENCE FROM N.A. (ISOFORM DELTA).
MEDLINE=98279152; PubMed=9616127;
              EMBL;
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                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
D1SEASE: Defects in PVRI1 are a cause of cleft lip/palate-ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI responsible for allelic forms known as Margarita island ect dysplasia [MIM:225060] and Zlotogora-Ogur syndrome. Gyplasia [MIM:225060] and Zlotogora-Ogur syndrome. SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like C2-type domains. SIMILARITS: NAME=PROW, NOTE=PROW 2:45-49[2001].
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                                                                                                                                                                                                                                                                                                                                                             www-"http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm"
AF060231; AAC23798.1;

AV29539; AAC33124.1;

AF252867; AAC16648.1;

AF196768; AAC16648.1;

AF196779; AAC16648.1;

AF196771; AAC16648.1;

AF196771; AAC16648.1;

AF196774; AAC16649.1;

AF196769; AAC16649.1;

AF196779; AAC16649.1;

AF196770; AAC16649.1;

AF196770; AAC16649.1;

AF196772; AAC16649.1;

AF196772; AAC16649.1;

AF196772; AAC16649.1;

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AF196772; AAC16649.1;

AF196772; AAC16649.1;

AF196772; AAC16649.1;
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F., Avitabile E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence=VSP_002626,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 simplex virus (HSV) receptor positively and negatively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      poliovirus receptor-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSP_002627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eisenberg
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Best Local Sim
Matches 104;
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GO; GO:0014895; F:ccell adhesion receptor activ
GO; GO:0015026; F:coreceptor activity; TAS.
GO; GO:0015026; F:coreceptor activity; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003396; Ig-v.
Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 2.
Cell adhesion; Immunoglobulin domain; Receptor
Repeat; Glycoprotein; Signal; Alternative spli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat; Glycoprotein; SIGNAL 1 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225060;
  244
                    222
                                      191
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                                                                                           114
                                                                                                              78
                                                                                                                               <u>ი</u>
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                                                                                                                                                         Similarity
                                                                                QESYTTITVLVPPRNLMIDIQKD-TAVEGEEIEV---NCTAMASKPATTIRWFKGNKELK
             QYKPQVHIQ---MTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGP
                                                                       RESQLNLTVMAKPTNWIEGTQAVLRAKKGQDDKVLVATCTSANGKPPSVVSW---ETRLK
                                                                                                                           IQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPP--
  QYEPEVTIEGFDGNWYLQRMD---
                                     GEAEYQEIRNPNGTVTVISRYRLVPSREAHQQSLACIV
                                                                                                              VAIYNPSMGVSVLAPYR
                                                                                                                                                                                     517
                                                                                                                                                                                                      459
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                                                                                                                                                                                                                                                                                                                            Conservative
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                                                    SDMYTVTSQLMLKVHKEDDGVFVICQVEHPAVTGNLQTQRY----LEV
                                                                                                                                                                                    57158
                                                                                                                                                         11.5%;
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                                                                                                          ----ERVEFLRPSFTDGTIRLSRLELEDEGVYICEFATFPTGN
                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                    IG-LIKE V-TYPE.
IG-LIKE C2-TYPE |
IG-LIKE C2-TYPE |
IG-LIKE C2-TYPE |
POLY-GLY.
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O'CLUNC
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Missing (i)
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N-LINKED
                                                                                                                                                                                                                                                                                                                                                                      N-LINKED
                                                                                                                                               Score 252.5; DB 1;
Pred. No. 7e-11;
9; Mismatches 155;
                                                                                                                                                                                Missing (In isoform Alpha).
/FTId=VSP 002627.
; DF34C8AEC893EE6D CRC64;
                                                                                                                                                                                                                   FPYTPSPPEHGRRAGFVPTAIIGGVAGSILLVLIVVGGIVV
ALRRRHTFKODYSTKUHVYGNGYSKAGIPQHHPPMAQNLQ
YPDDSDDEKKAGPLGGSSYEESEEEEEGGGGERKYVGGPHP
-> KPRPQRGLGSARLLAGTVAVFLLIVAVLTVFFLYNRQ
QKSPFETDGAGTDQPLSQKPEPSPSRQSSLVPEDIQVVHLD
PGRQQQEEEDLQKLSLQPPYYDLGVSPSYHPSVRTTEPRG
ECP (in isoform Alpha).
                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . . . EFPYTPSPPEHGRRAGPV ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POLIOVIRUS RECEPTOR RELATED PROTEIN EXTRACELLULAR (POTENTIAL).
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POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (PO
                                                                                                                                                                                                               /FTId=VSP
                                                                                                                                                                                                                                                                                                                isoform Gamma).
-VKLTCKADANPPATEYHWTTLNGSLPKGVEAQNR
                                                                                                                                                                                                                                                                                                                               GLCNAC.

GECNAC.

GECNAC.

GECNAC.

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GECNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane,
                                                                                                                                                                                                                                                                                             Gamma).
                                                                                                                                                               Length
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.) (POTENTIAL).
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                                     -NYHMDRFKESLTLNV
                                                                                                                                                                 517;
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                                                                                                                                               Gaps
                  278
                                                                       190
                                                                                         169
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VR2_MOUSE

VR2_MOUSE

ID PVR2_MOUSE

AC P33507; 062096;

AC P33507; 062096;

DT 01-0CT-1993 (Rel. 27, Created)

DT 16-0CT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Poliovirus receptor related protein 2 precursor (Mur

DE entry protein B) (mHveB) (Nectin 2) (Poliovirus rec

PVELIZ OR PVS OR PVR OR MPH.

""FGulus (Mouse).

""FGulus (Mouse).

""TOA; Chordata; Craniata; Vertebrat;

""TOA; Sciurognathi; Murid
   ALD CARRAR RANGE OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF COLOR OF C
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                                                                                                                                                                                    Strausberg R.I., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Altabeton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Altabeton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Altabeton M.J., Botares G.J., Abramson R.D., Mullahy S.J.,

Altabeton E., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Altabeton E.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., McHton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Altabeton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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Altabeton E., Crimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

"Inman and mouse cDNA sequences.",

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      MEDLINE=99214397; PubMed=10196354;
Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
"The murine homolog (Mph) of human herpesvirus entry protein B (Hymaniare homolog (Mph) of human bernessimus entry of pseudorabies virus but not herpes simplex virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aoki J., Koike S., Ise I., Sato-Yoshida I "Amino acid residues on human poliovirus interaction with poliovirus";
J. Biol. Chem. 269:8431-8438(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=94179228; PubMed=8132569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM ALPHA)
MEDILINE=92219365; PubMed=1560525;
Morrison M.E., Racaniello V.R.;
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poliovirus receptor gene.";
J. Virol. 66:2807-2813(1992).
mediates entry of pseudorabies types 1 and 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM STRAIN=FVB/N;
                                                                                                            CHARACTERIZATION.
MEDLINE=99214397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A. (ISOF
VB/N; TISSUE=Col
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hi; Muridae; Murinae; Mus
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                                                    (HveB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A38211;
PIR; A53437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:97822; Pvrl2.
InterPro; IPR007110; Ig-like
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virol. 73:4493-4497(1999).
- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative
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                                                                                                                                                                                                                                                                                              Similarity
                                                                 -NKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQL-----LNFSSSELKVSLTNVSIS
                                                                                                                               PTIPILPLILIL----IQETG-AQDVRVRVLPEVRGRLGGTVELPCHLLPPTTERVSQVT
                                                                                                                                                                                          PGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEV---ATISCQV---
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22.6%;
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IG-LIKE C2-TYPE 1.
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N-LINKED (GLCNAC. . . .) (POTENTIAL).
ANDEDSEZELEGPPSYKPPTPKAKLEEPEMPSQLFTLGA
SEHSPVKTPYPDAGVSCADQEMPRYHELPTLERESGPLLGA
ASHSPVKTPYPDAGNSSDVGPLWGAVGGTLUVILLAGGFU
ALLILRGRRRRKSPGGGGNDGDRGSYDPKTQVFGNGGPVFW
RSASPEPRRPGGREEDBESEEBKKAEBGLMLPPHESPKDDM
RSASPEPRRPGGREEDBESEEBKKAEBGLMLPPHESPKDDM
                                                                                                                                                                                                                                                                   61;
      - FGVDFPNSQFSKDRLSFVRARPETNADLRDATLAFRGLRVE
                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (i
/FTId=VSP
                                                                                                                                                                                                                                                                                                  Score 243;
Pred. No. 3.
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLIOVIRUS RECEPTOR RELATED EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESHLDGSLISRRAVYV (in isoform
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Missing (in isoform Alpha).

/FTId=VSP 002631.

0ED71BFA2B231BBE CRC64;
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3.5e-10;
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, spleen, kidney,
                                                                                                                                                                                                                                                                   162;
                                                                                                                                                                                                                                                                                                                             Length 530
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RA Strausberg R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Schammen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K., RA Lischul S.F., Zeeberg B., Buetcow K.H., Wang J., Hsieh F., RA Schaplecon M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Woldin T.B., Toshiyuki S., Carninci P., Prange C., RA RA RAS.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Raha S.S., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., RA Roharde S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaln D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villaln D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Villaln D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA RA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA RA Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM ALPHA).

MEDLINB=98321161; PubMed=9657005;
Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
Warner M.S., Geraghty R.J., Cohen G.H., Spear P.G.;
Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
"A cell surface protein with herpesvirus entry activity (HveB)
susceptibility to infection by mutants of herpes simplex virus
1, herpes simplex virus type 2, and pseudorables virus.";
Virology 246:179-189(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           092652; 075455; 096179;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Poliovirus receptor related protein 2 precursor
mediator B) (HyeB) (Nectin 2) (CD112 antigen).
PVRL2 OR PRR2 OR HYEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM ALPHA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PVR),
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human PRR2 gene
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E=95347610; PubMed=7622062;

F., Dubreuil P., Mattei M.-G., Devilard E., Log
uman PRR2 gene, related to the human poliovirus
is the true homolog of the murine MPH gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEEPILLPVTLSVRYPPEVSIS-GYDDNWYLGRSEAI-LTCDVRSNPEPTDYDWSTTSGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMASKPATTIRWFKG-NKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEGNYTCEFATFPNGTRRGVTWLRVIAQPEN-----HAEAQEVTIGPQSVAVARCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pegryfcqlytpe--pqesyttitylvpprylmidiqkdtavegeeiev-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTTTTLTIITDSRAGEEGTIGAVDHAVIGGVVAVVV 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGATGG-----IIGGIIAAII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rador
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235
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EMBL; X80038; CAA56342.1; -...
EMBL; AF058448; AAC33797.1; -...
EMBL; BCC03091; AAH03091.1; -...
EMBL; BCC03091; AAH03091.1; -...
EMBL; AF044968; AAC82348.1; JOIN
EMBL; AF044962; AAC82348.1; JOIN
EMBL; AF044964; AAC82348.1; JOIN
EMBL; AF044964; AAC82348.1; JOIN
EMBL; AF044967; AAC82348.1; JOIN
EMBL; AF044967; AAC82348.1; JOIN
EMBL; AF044967; AAC82348.1; JOIN
EMBL; AF044967; AAC82348.1; JOIN
EMBL; AF044967; AAC82348.1; JOIN
EMBL; AF050154; AAD02503.1; -...
PIR; I68093; I68093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEREC1.";

DNA Seq. 9:89-101(1998).

-I- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1 PSEUDORABIES VIRUS) ENTRY INTO CELLS.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;
            DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DISULFID
DISULFID
                                                                                                                                              Repeat;
                                                                                                                                                                                                                    GO; GO:0005886; C:plasma membrane; GO; GO:0015026; F:coreceptor activi InterPro; IPR007110; Ig-like. InterPro; IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-gorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Generation and : human and mouse of Proc. Natl. Acad [4]
                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                          MIM;
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MEDILINE-99449047; PubMed=10520737;
Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K.,
Ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.;
"Sequencing of 42kb of the APO E-C2 gene cluster I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing
Submitted (
[5]
                                                                                                                                                                                              Pfam; PF00047; ig; 2.
SMART; SM00409; IG; 1
                                                                                                                                                                                                                                                                                       Genew; HGNC:9707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 31-538 FROM N.A.
Yoshiura K., Murray J.C.;
Yoshiura K., Murray J.C.;
"A transcriptional map in the region of 19q13
sequencing and exon trapping,";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                   SMART; SM00409; IG; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin domain; Rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE SECCIFICITY: Übiquitous.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
DATABASE: NAME=PROW; NOTE=PROW 1:74-77(2000);
NWW="http://www.ncbi.nlm.nih.gov/prow/guide/204270028_g.htm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Alpha;
IsoId=Q92692-2;
                                                                                                                                                                                                                                                                             600798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q92692-1; Sequence=Displayed,
                                                                                                                                                         Alternative
             361
361
382
382
382
162
261
183
283
        Acad.
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                                                                                                                                                                                                                                                                                       PVRL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence=VSP_002628,
                                                                                                                                                                   Receptor;
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; JOINED.
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POLIOVIRUS RECEPTOR RELAT:
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                brane; TAS.
                                                                                                                                           POTENTIAL
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                                                                                                                                                                   Transmembrane;
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                                                                                                                 CEPTOR RELATED (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSP_002629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in no way
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SEQUENCE FROM N.A. TISSUE=Kidney; MEDLINE=93059651;

PubMed=1331508 (ISOFORMS

ALPHA

AND

Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;

Poliovirus receptor PVR OR PVS.

precursor.

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Best Local :
                                                                                                                   PVR CERAE STANDARD; PRT; 417 AA.

P32506;
01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
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CARBOHYD
VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABLQDATLALHGLTVEDEGNYTCEFATEPKGSVRGMTWLRVIAKPKN-QAEAQKVTFSQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNP
                                                                                                                                                                                                                                                                                                                                                  PPTTTTTTTTTTTTLTIITDSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRY
                                                                                                                                                                                                                                                                                                                                                                        DWSTTSGTFPTSAVAQGSQLVIHAVDSLFNTTFVCTVTNAVGMGRAEQVIFVRETPNT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----ELKVSLTNVSISDEGRYFCQLYTDP---PQESYTTITVLVPPRNLMIDIQKDTAVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPGLYISLVTWQRPDAPANHQNV--AAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTE
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324
479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NROTIYERDERPLKDSRE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 238.5;
Pred. No. 7.6e
63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

NTAGAGATGGIIGGIIAGNIATAVAATGILICRQOKKEQTL

NTAGAGATGGIIGGIIAGNIATAVAATGILICRQOKKEQTL

QGAEEDDEBGEPSYKEPTPKAKLEAQEMPSQLFTLGASEH

SPLKTPYFDAGASCTEQEMPRYHELPTLEERSGPLHPGATS

LGSPIP -> RASPRDVGPLVWGAVGGTLLVLLLLAGGSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP_002628.
Missing (in isoform Alpha).
/FTId=VSP_002629.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3AE4F83E92F6F624 CRC64;
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Matches 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                    Repeat;
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PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         has no putative N-glycosylation immunoglobulin-like domain.";
                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 3
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D12611;
EMBL; D12612;
                                                                                                                                                                      CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P32506-2; Sequence=VSP_002622, VSP_002623;
SIMILARITY: Contains 1 immunogTobulin-like V-type domain.
SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted (isoforms beta ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Delta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Alpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                   ,, D12611; BAA02136.1; -.
,, D12612; BAA02137.1; -.
A44194; A44194.
B44194, B44194.
                                           107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P32506-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P32506-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=P32506-1; Sequence=Displayed;
   ω
                      ,
                                                     Similarity
                                                                                                                                                                                                                                                                                                                              Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ise I., Sato Y., Yonekawa H., GOLUH O., NUMBER TO THE African green monkey poliovirus receptor that gene for the African gite in the functional N-terminal
                       AAPPGLRLLLLLLSAAALIPTGDGQNLFTKDVTV--IEGEVATISC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66:7059-7066(1992)
                                                                                   417
                                                                                                                            Conservative
                                                                                                        393
                                                                                   AA;
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                                                                                                                            LLLTLLELSWPPPGTGDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHV
                                                                                                                                                                                                                                                                                                                              splicing
                                                                                     45464 MW;
                                                    10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence=Not
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                                           68;
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                                                                                                                                     IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
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                                                             Score
                                                                                              /FTId=VSP_002622.
Missing (in isoform
/FTId=VSP_002623.
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POLIOVIRUS RECEPTOR.
EXTRACELLULAR (POTENTIAL).
                                                     Pred.
                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
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                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      described;
                                                    237; DB 1;
No. 7.1e-10;
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                       QVNKSDDSVI
                                            90;
                                                                                                                               Delta).
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                                           Gaps
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RESULT
PVR1_MC
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Poliovirus receptor related protein 1 precursor mediator C) (HveC) (Nectin 1).
PVRL1 OR PRR1 OR HVEC.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=20541977; PubMed=11090177;
Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;

"Striking similarity of murine nectin-lalpha to human (HveC) in sequence and activity as a glycoprotein D realphaherpesvirus entry.";

O, Virol. 74:11773-11781(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Lecocq E., Dubreuil P., Campadelli-Fiume G.;
"The murine homolog of human mectini delta serves as a spronspecific mediator for entry of human and animal alpha in a pathway independent of detectable binding to gD.";
Proc. Natl. Acad. Sci. U.S.A. 97:4887-4872(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                         Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databi-
-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RI
ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES
                                                                                                                                                                            STRAIN-Swiss Webster;
Zhan J., Wimmer E.;
Zhan J., Wimmer E.;
"Mouse nectin-1 (mPRR1), a herpesvirus receptor, is
floor plate during embryogenesis, suggesting a role
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                           development.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=20243787; PubMed=10781093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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CELLS.
SUBUNIT: Interacts with HSV SUBCELLULAR LOCATION: Type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         393
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Sciurognathi; Muridae; Murinae;
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I membrane protein.
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GO; GO:0005913; C:cell-cell adherens junction; ID;
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0004872; F:receptor activity; IDA.
InterPro; IPR007110; Ig-like.
R InterPro; IPR003599; Ig.
R Pfam; PF00047; ig; 2.
R SMART; SM00409; IG; 2.
R PROSITE; PS50835; IG_LIKE; 2.
R PROSITE; PS50835; IG_LIKE; 2.
GN Repeat; Glycoprotein; Signal.
ON Repeat; Glycoprotein; Signal.
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EMBL; AF270977; AAF76195.1; -.
EMBL; AF297665; AAG22808.1; -.
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VTVISRYRLVPSREAHROSLACIV-----
                                                                                               YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRY-----LEVQYKPQVHIQMTYPL
                                 EGF--DGNWYLQRTDVKLTCKADANPPATEYHWTTLNGSLPKGVEAQNRTLFFRGPITYS
                                                                                                                                  --IEGTRAVLRARKGQDNKVLVATCTSANGKPPSAVSW---ETRLKGEAEYQEIRNPNGT
                                                                                                                                                         IDIQKDTAV----EGEEIEV----NCTAMASKPATTIRWFKGNKELKGKSEVEEW---SDM
                                                                                                                                                                                 PPYEKRVEFLRPSFIDGTIRLSGLELEDEGMYICEFATFPTGNRESQLNLTVMAKPTNW-
                                                                                                                                                                                                        PLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPP--QESYTTITVLVPPRNLM
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                                                                                                                                                                                                                                                                                   57064 MW;
                                                                                                                                                                                                                                              10.7%;
                                                          -ELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINN-LNKT
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Pred. No. 1.1e-09
9; Mismatches 14:
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BY SIMILARITY.
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N-LINKED (GLCNA
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
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                                                                                                                                                                                                                                                                                L -> P (IN REF. 1).
N -> D (IN REF. 1).
P -> PP (IN REF. 2).
S -> G (IN REF. 3).
FFFF608EB5FFB7AOF CRC64;
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                                                                                -NYHLDRFRESLTLNVQYEPEVTI-----
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RESULT 7
NCA1_XENLA
ID NCA1_XEN
AC P16170;
    Pfam; PF00041; fn3; 2. Pfam; PF00047; i9; 5. SMART; SM00060; FN3; 2. SMART; SM00408; IGC2; 5. PROSITT; PS50835; IG LIKE; 5 Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990
15-MAR-2004
Neural cell
                                                                                                                                                           PIR;
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                             -!- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND EARLY NEURAL DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLULAR LOCATION: Type I membrane protein
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krieg P.A., Sakaguchi D.S., Kintner C.R.;
"Primary structure and developmental expression cytoplasmic domain form of Xenopus laevis neural molecule (NCAM).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                      ISOId=P16170-2; Start Start Start Specificity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 17:10321-10335(1989)
-I- FUNCTION: This protein is a cell add
neuron-neuron adhesion, neurite fass
neurites, etc.
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                                                                                                                                                                          EMBL; M25696; AAA49909.1;
                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS N-CAMEDLINE=90098871; PubMed=2481269;
                                                                                                                                               HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8355
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                                                                                     InterPro;
                                                                                                    [nterPro;
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                                                                                                                                nterPro;
                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains 5 immunoglobulin-like SIMILARITY: Contains 2 fibronectin type II:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=N-CAM 180;
IsoId=P16170-1; Sequence=Displayed;
Name=N-CAM 140;
                                                                                                                                          ; P56276; IJXLNL.
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                                                                               IPR008957; FN III-like.
IPR003961; FN III.
IPR003110; IG-like.
IPR003598; IG-c2.
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(Rel. 14, Last sequence update)
(Rel. 43, Last annotation update)
adhesion molecule 1, 180 kDa isoform
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 Glycoprotein;
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Transmembrane; Repeat;
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in neuron
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Best Local
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        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequ
10-OCT-2003 (Rel. 42, Last anno
Neurotrimin precursor.
Mus musculius (Mouse).
Eukaryota, Metazoa, Chordata, C
Mammalia, Eutheria, Rodentia, S
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28-FEB-2003
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                                                                                                                                         EFILVQADTPSS---PAIRKVEPYSSTVMIVFDEPDSTGG
                                                                                                                                                             DYMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIITDSRAG
                                                                                                                                                                               PR-AAVTWFRDGQLLPSSNFSNIKIYSGPTSSSLEVNPDSENDFGNYNCTAINTIGHEFS
                                                                                                                                                                                                    PQPVMVTWVRVDDEMPQH-----AVLSGP----NLFINNLNKTDNGTYRCEASNIVGKAHS
                                                                                                                                                                                                                       TDAGEYFCIASNP-IGVDWQAM-YFEVQYAPKIR----GPVVVYTWEGNEVNITCEVFAH
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Last sequence up
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IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
HEPARIN-BINDING (POTENTIAL).
HEPARIN-BINDING (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTEN
MISSING (in isoform N-CAM 140
/FTId=VSP 002589.
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                                                                                                                                                                                                                                                                                                                                                                                            Score 234; DB 1;
Pred. No. 3.9e-09;
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          Craniata; Vertebrata; Sciurognathi; Muridae;
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                                                 update)
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                     Euteleostomi;
           Murinae;
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RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Schepteron M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

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Kim T.H., Choi S.C., Kim J.,
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STRAIN=C57BL/6; TISSUE=Eye;
STRAIN=257BL/6; TISSUE=Eye;
MEDLINE=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
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SMART; SM00409; IG; 3.

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Submitted (JUN-2000) to the
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snmen C.M., Schuler G.D
naefer C.F., Bhat N.K.,
Hsieh F.,
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                                     Koike S., Horie H., Ise I., Okits
Takeuchi K., Takegami T., Nomoto
"The poliovirus receptor protein
and secreted forms";
EMBO J. 9:3217-3224(1990).
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Cell 56:855-865(1989).
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01-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Poliovirus receptor precursor (CD155 antigen)
PVR OR PVS.
      SEQUENCE
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                                                                                                                                                                                                          Submitted [3]
                                                                                                                                                                                                                                                  Racaniello
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-89168426; PubMed=2538245;
Mendelsohn C.L., Wimmer E., Racaniello V.R.;
"Cellular receptor for poliovirus: molecular
sequence, and expression of a new member of t
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Zibert A., Wimmer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kodoylanni V., Severin J., Ge Y., Grable L., Kvistad E., Shannon M., Brower A., Olsen A.S., Smith L.M.; "Sequence analysis of a 1Mb region in 19q13.2 containing gene cluster."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: THE V-TYPI
VIRUS BINDING AND UPTAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91239515; PubMed=1851992;
Koike S., Ise I., Nomotto A.;
"Functional domains of the poliovirus
Proc. Natl. Acad. Sci. U.S.A. 88:4104-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function of the human poliovirus J. Virol. 66:7368-7373(1992).
                                                                                                                                                                                         SIMILARITY: Contains SIMILARITY: Contains DATABASE: NAME=PROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell.
SUBCELLULAR LOCATION: Type
Subcellular Location: Type
                                                                                                                                                                 SIMILARITY: Contains 1 immunoglobulin-like V-type do SIMILARITY: Contains 2 immunoglobulin-like C2-type d DATABASE: NAME=FROW, NOTE=CD guide CD155 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd155.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                       delta). Secreted (isoforms beta and gamma).
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                  IsoId=P15151-3; Sequence=VSP_002618,
                                                                                                                                                                                                                                                                                               IsoId=P15151-4; Sequence=VSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF CARBOHYDRATE-LINKAGE 59689; PubMed=1331527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the virus
                                                                                                                                                                                                                                                                                                                                                                        Sequence=VSP_002617;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence=Displayed;
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DOMAIN IS NECESSARY
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(See http://www.isb-sib.ch/announce/
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GO; GO:0005737; C:cytoplasm; TAS.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0006612; C:integral to membrane; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0007125; F:invasive growth; TAS.
InterPro; IPR003106; Ig-like.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 3.
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S12048;
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512048; RWHUPA.
; HGNC:9705; PVR.
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YKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
                                                                                                                                 LYTDPPQESYTT---ITVLVPPRNLMIDIQKDTAVEGEEIEV-NCTAMASKPATTIRWFK 163
                                              DLGGMPNTSQVPGFLSGTVTVTSLWILVPSSQVDGKNVTCKVEHESFEKPQLLTVNLTVY
                                                                         GNKELKGKSEVEEM-SDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
                                                                                                         LFVTFPQGSRSVDIWLRVLAKPQN-TAEVQK-VQLTGEPVFMARCVSTGGRPPAQITWHS
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IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 2.

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Pred. No. 1.8e
53; Mismatches
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TEHASASA -> EHHQS
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/FTId=VAR_011736.
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Missing (in isoform Delta)
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InterPro; IPR003598; Ig_c2.
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SMART; SM00408; IGC2; 2.
PROSITE; P850835; IG_LIKE; 3.
                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www ich air or send an email to licensease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Struyk A.F., Canoll P.D. Salzer J.L.;
"Cloning of neurotrimin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurotrimin precursor (GP65).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratt
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MEDLINE=95198094; PubM
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(Rel. 35, Last sequence update)
(Rel. 42, Last annotation update)
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domain; Cell adhesion;
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(GLCNAC.)
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HUMAN
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Li G., Jin J., Tan X., Hu S., Yuan J., Qiang B.;
"Cloning and identification of human neurotrimin full length cDNA."
Submitted (FEB-199) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Neural cell adhesion molecule.
-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-i- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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   EMBL; AF126426; AAF37591.1;
MIM; 607938; -.
GO; GO:0008038; P:neuronal o
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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 GO:0008038; P:neuronal
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RESULT 12
NCM2_MOUSE
ID NCM2_M
AC 035136
DT 15-UIL
DT 15-UIL
DT 10-CCT
DE Neural
DE Adhesi
GN NCAW2
OC Eukary
OC Mammall
RN (1)
RN (1)
RP SEQUEN
RC STRAIN
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Best Local S
Matches 85
                         Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10090;
[1]
                                                                    NCM2 MOUSE STANDARD; PRT; 837 AA.
035136; 035962;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Neural cell adhesion molecule 2 precursor (N-CAM
adhesion molecule) (R4B12).
Nus musculus (Mouse).
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 SEQUENCE FROM STRAIN=BALB/c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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I.A. (ISOFORMS LONG AND SHORT)
TISSUE=Olfactory neuroepithel
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2 321
2 344
                                               Chordata;
Rodentia;
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Ig_c2.
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IG-LIKE C2-T
IG-LIKE C2-T
IG-LIKE C2-T
POTENTIAL.
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Pred. No. 2.1e-09;
7; Mismatches 135
                                               Craniata; Vertebrata;
Sciurognathi; Muridae;
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DA4D12C295ABBB3A
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C2-TYPE 1.
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C2-TYPE 3.
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                                               Euteleostomi;
Murinae; Mus
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neuroepithelium;

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EMBL; AF001287; AAB69125.1; -.
EMBL; AF001286; AAB69124.1; -.
EMBL; AF001619; ACC5375.1; -.
MGD; MGI:97282; Ncam2.
InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-c2.
CARBOHYD
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                                                                                                                                                                                                                    Pfam; PF00041; fn3; 2.

Pfam; PF00047; i9; 5.

SMART; SM00060; FN3; 2.

SMART; SM000608; IGC2; 5.

PROSITE; PS50835; IG_LIKE; 5.

Cell adhesion; Transmembrane; GPI-anchor; A

Immunoglobulin domain; Signal; GPI-anchor; A
                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a content the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restricts use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM SHORT)
STRAIN=C57BL/6J; TISSUE=Olfactory
MEDLINE=97476194; PubMed=9334170;
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"Identification of a novel neural cell adh
with a potential role in selective axonal
J. Biol. Chem. 272:26083-26086(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            axons.";
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Yoshihara Y., Kawasaki M., Tamada
                                                                                         DOMAIN
                                                                                                                                                                                                                 SIGNAL
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FUNCTION: May play important roles in selective for grone-to-zone projection of the primary olfactory subcellular Location: Type I membrane protein (le attached to the membrane by a GPI-anchor (short in ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Expressed in subsets of both olfactory vomeronasal neurons in a zone-specific manner. SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Long;
IsoId=O35136-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
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A new member of the neural cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=035136-2;
  17:5830-5842(1997)
  a novel neural cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence=Displayed;
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                                                                                       CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
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IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 1.
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 1.
PROBABLE.
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(long isoform)

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RESULT 13
NCM2 H
AC 015394
DT 15-UUL
DT 15-UUL
DT 10-OCT
DE Neural
GN NCAM2
OC Mammall
GN NCBLT
RN [1]
RP SEQUEN
RC TISSUE
RX FELICATI
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Best Local S
Matches 90
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15-JUL-1998 (Rel
10-OCT-2003 (Rel
Neural cell adher
NCAM2 OR NCAM21.
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VARSPLIC
CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.

MEDLINE=22660472; PubMed=12754519;

Zhang H., Li X.-J., Martin D.B., Aebersold R.;

"Identification and quantification of N-linked glycop hydrazide chemistry, stable isotope labeling and mass Nat. Biotechnol. 21:660-666(2003).

Nat. Biotechnol. 21:660-666(2003).

-i- FUNCTION: May play important roles in selective for zone-to-zone projection of the primary olfactory
                                                                                                                                                                                                                   MEDLINE=97369930, PubMed=9226371;
Paoloni-Giacobino A., Chen H., Antonarakis S.E.;
"Cloning of a novel human neural cell adhesion molecule that maps to chromosome region 21q21 and is potentially Down syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
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(Rel. 36, Last sequence update)
(Rel. 42, Last annotation update)
adhesion molecule 2 precursor (N-CAM
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TIPNGLGLGAIIGLGVAALLLLILVTIDVSCFFIRQCGLLMC
ITRRMCGKXGGSGKSKELEEGKAAYLKDGSKEPIVENRTE
DERITMHEDGSPVNEPNETTPLTEPEKLPLKEENGKEVLNA
ETIEIKVSNDIIQSKEDDIKA -> NCCEANKGENGGQSWH
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Pred. No. 1.2e
51; Mismatches
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Catarrhini; Hominidae; Homo
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R MIM; 602040; ...

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:0015086; C:plasma membrane; TAS.

R GO; GO:0007158; P:neuronal cell adhesion; TAS.

R InterPro; IPR009957; FN III-like.

IN InterPro; IPR003961; FN III-like.

R InterPro; IPR003961; FN III-like.

NR InterPro; IPR0037110; Ig-like.

NR InterPro; IPR003598; Ig-22.

NR Pfam; PF00047; fn; 5.

DR Pfam; PF00047; ig; 5.

DR SMART; SM004060; FN3; 2.

DR SMART; SM00408; IG-21, 5.

DR PROSITE; PS50835; IG_LIKE; 5.

Cell adhesion; Transmembrane; Glycoprotein; Rep.

KW Central Communoglobulin domain; Signal.

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MIM; 602040;
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nes 115; Conser
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                                          LMIDIOKD---TAVEGBEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTV--
                                                                                                       TTISDNRLAML---
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                                                                                                    -ANNNLQILNINKSDEGIYRCEGRVEARGEIDFRDIIVIVNVPPAI
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                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 5.

IG-LIKE C2-TYPE 1II 1.

IIBRONECTIN TYPE-III 2.

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7; Mismatches 180
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                                                                                                                                                                                                                                                                                                        180;
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                                                                                                                                                                                                                                                                                                                                                  Length 837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in
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     BENEKYILKG
                                                                                                                                                                                                                                                                                                   Gaps
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EMBL; M76710; AAA49910.1; -
PIR; UN0635; JN0635.
HSSP; P56276; ITLK.
InterPro; IPR008957; FN III
InterPro; IPR003961; FN_III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2_XENIA

NCA2_XENIA

P36335;

01-JUN-1994

01-JUN-1994

15-MAR-2004

Neural cell
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laevis are expressed during Gene 127:243-247(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93273239; PubMed=7684721;
Tonissen K.F., Krieg P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCAM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                             IsoId=P36335-1; Sequence=Displayed; SIMILARITY: Contains 5 immunoglobulin-like C2-type domains. SIMILARITY: Contains 2 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELULIAR LOCATION: Type I membrane protein
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: This protein is neuron-neuron adhesion, ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neural-cell adhesion molecule (NCAM)-encoding genes in a sare expressed during development and in adult tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLCL-----LILLGRYFAR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRXLEVQYKPQVHIQMTYPLQGLTREG
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(Rel. 29, Last sequence update)
(Rel. 43, Last annotation update)
adhesion molecule 2, 180 kDa isof
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FN_III.
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Pfam; PF00047; ig; 5.

SMART; SM00060; FN3; 2.

SMART; SM00408; IGC2; 4.

PROSITE; PS50835; IG_LIKE; 5.
Q9QZS7;
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DOMAIN
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InterPro; IPR003598; Ig_c2.
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                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                 S-AAVSWFRDGQLLPSSNFSNIKIYNGPTFSSLEVNPDSENDFGNYNCSAVNSIGHESSE
                                                                                                                                                                                                                                 ISFNEDKSEMTIYRVEKEDEAEYSC-IANNQAGEAEAIVLLKVYAKPKMTYVENKTTVEL
                                                                                                                                                                                                                                                                      KDIQVIVNVPPLIQARQIRVNATANMDESVVLSCDADGFPDPEISWLKKGEPIEDGE-EK
                                                                             FILVQADTPSS---PAIRKVEPYSSTVMIVFDEPDATGG
                                                                                              YMLYVYDPPTTIPPPTTTTTTTTTTTTLTIITDSRAG
                                                                                                                                   QPVMVTWVRVDDEMPQH-----AVLSGP----NLFINNLNKTDNGTYRCEASNIVGKAHSD
                                                                                                                                                                       DGALALICOAEH PAALGALICA KANDAKA KANDAKA KALOALIO KANDALA KANDALA KANDALA KANDALA KANDALA KANDALA KANDALA KANDA
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                                                                                                                                                                                                              ESIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVT-----SQLMLKVHKED
                                                                                                                                                                                                                                                  LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG
                                                                                                                                                                                                                                                                                     KDVTVIEGEVATISC---QVNKS---DDSVIQLLN----PNRQTIYFRDFRPLKDSRFQL
                                                                                                                                                      DAGEYFCVASNP-IGVDMQAM-YFEVQYAPKIR----GPVVVYTWEGNPVNITCDVLAHP
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41
136
232
232
323
420
219
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341
441
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472
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                             STANDARD;
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           Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.

CYTOPLASNIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 4.

IG-LIKE C2-TYPE 5.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

HEPARIN-BINDING (POTENTIAL).

HEPARIN-BINDING (POTENTIAL).
  sequence update
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N-LINKED
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N-LINKED
N-LINKED
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                                                                                                                                                                                                                                                                                                                   Score 222;
Pred. No. 2.
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                             PRT;
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                             1242 AA
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(GLCNAC...)
(GLCNAC...)
(GLCNAC...)
                                                                                                                                                                                                                                                                                                                   DB 1;
.9e-08;
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                                                                                              346
                                                                                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                                                                                           Indels
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(POTENTIAL).
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InterPro; IPR008957; FN_III-like.
InterPro; IPR00361; FN_III.
InterPro; IPR00351; FN_III.
InterPro; IPR003598; IG_C2.
Pfam; PF00041; fn3; 1.
Pfam; PF00041; fn3; 1.
Pfam; PF00047; fn3; 1.
SMART; SM00060; FN3; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
Cell adhesion; Transmembrane; Signal; Glycoprotein;
Cell adhesion; Transmembrane; Signal; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH CD2AP AND NPHS2:
MEDLINE=21590460; PubMed=11733557;
Schwarz K., Simons M., Reiser J., Saleem M.A., Faul C., Kriz
Shaw A.S., Holzman L.B., Mundel P.;
Shaw A.S., Holzman L.B., Mundel P.;
"Podocin, a raft-associated component of the glomerular slit
diaphragm, interacts with CD2AP and nephrin.";
J. Clin. Invest. 108:1621-1629(2001).
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Shih N.Y., Li J., Cotran R., Mundel P.,
"CDZAP localizes to the slit diaphragm
novel C_terminal domain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                              <u>8</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF168466; AAF03368.1; -. MGD; MGI:1859637; Nphs1.
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Mammalia; Eutheria; Rodentia;
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"Nephrin localizes to the slit pore of the glomerular epithelial
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                                                                                                                                                 mmunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005515; F:protein binding;
GO:0007254; P:JNK cascade; IDA.
GO:0000165; P:MAPKKK cascade; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCEILULAR LOCATION: Type I membrane protein (Potenti at podocyte slit diaphragm between podocyte foot proce TISSUE SPECIFICITY: Expressed in kidney glomeruli. PTM: Phosphorylated on tyrosine residues (By similarit SIMILARITY: Belongs to the immunoglobulin superfamily. SIMILARITY: Contains 8 immunoglobulin-like domains. SIMILARITY: Contains 1 fibronectin type III domain.
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Sciurognathi; Muridae;
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IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 8.
FIBRONECTIN TYPE-III.
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Q8r5m8 mus
Q9by67 homo
Q7tn11 mus
Q8n2f4 homo
Q9d6e7 mus
Q80vg4 mus
Q8cwb homo
Q9z2h8 mus
Q9gy14 mus
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                 PSEQUENCE (NATUYAMA T., Murakami Y.;

RTRAIN=129/SvJ;

RA Fixami T., Maruyama T., Murakami Y.;

RT "Identification of murine orthologue of the TSLC1 gene.";

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RT "Jdentification of murine orthologue of the TSLC1 gene.";

RT "Jdentification of murine orthologue of the TSLC1 gene.";

RMSJ; AF43463; AAL86736.1; -.

R GO; GO:0045202; C:synaptic vesicle; IDA.

RR GO; GO:0045215; F:calcium-independent cell adhesion molecule

RGO; GO:0005515; F:protein binding; IPI.

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0005515; P:protein binding; IPI.

GO; GO:0005515; P:protein binding; IPI.

RGO; GO:0005515; P:protein binding; IDA.

RR GO; GO:0005515; P:protein binding; IDA.

RR GO; GO:000515; P:protein binding; IPI.

RGO; GO:000515; P:protein binding; IDA.

RR GO; GO:000515; P:protein binding; IPI.

RGO; GO:000515; P:protein binding; IPI.

GO; GO:000515; P:protein binding; IDA.

RR GO; GO:000515; P:protein binding; IPI.

RGO; GO:00051; P:protein binding; IPI.

RGO; GO:00051;
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Best Local Similarity
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QBR4L1,
Q1-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor suprressor in lung cancer 1.
IGSF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Q8I0L3
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Q8CIJ4
Q80W68
Q91VT9
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Q9NQS3
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Q57349
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Q8bypi mus musculu
Q8bxj7 mus musculu
Q8bxj4 mus musculu
Q8bzp4 mus musculu
Q7zxxi xenopus lae
Q8r464 mus musculu
Q9p128 mus musculu
Q9p128 mus musculu
Q9p144 homo sapien
Q9y44 homo sapien
Q9y49 homo sapien
Q9yipi homo sapien
Q9yipi homo sapien
Q9ujpi mus musculu
Q9nyi5 homo sapien
Q8bsq8 mus musculu
Q9nqs3 homo sapien
Q8bipi mus musculu
Q9nqs3 homo sapien
Q8izq9 homo sapien
Q8izq9 homo sapien
Q9ilb7 mus musculu
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Q9v4y0 drosophila
Q8i013 caenorhabdi
O76518 caenorhabdi
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Q80w68 mus musculu
Q91vt9 mus musculu
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musculu sapien

Minimum Maximum

DB DB

seq length:
seq length:

Searched:

Scoring table: Sequence:

Title: Perfect score:

Run

on:

July

OM protein -

Database

Result No.

Score

Query Match

.; IDA.

2197 2176.9 2166 20057 2020.27 2020.1631 1631 15415 15415 1493 1493 1380.5 897

Gaps

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420 381 360 321 300 261

441

180

201

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                                              MGD; MGI:1889272; Igsf4.

GO; GO:0045202; C:synaptic junction; IDA.
GO; GO:0008021; C:synaptic vesicle; IDA.
GO; GO:0016347; F:calcium-independent cell ad
GO; GO:0015515; F:protein binding; IPI.
GO; GO:0007115; P:cell adhesion; IDA.
GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig_c2.
Pfam; PF00047; Ig; 3
SMART; SM00409; IG; 3
SMART; SM00409; IG; J.
PROSITE; PS50835; IG_LIKE; 3.
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                   SEQUENCE
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Sudhof T.C.;
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Mammalia; Eutheria;
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                 immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Mouse)
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                 AA;
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Rodentia;
                 48666 MW;
                                                                                                                                                                                                                                                                                                                                                                                       Mozhayeva M.,
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22, Last sequence update)
25, Last annotation update)
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Sciurognathi; Muridae;
                   5B336F23F1877497
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                   CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                       Kavalali E.T.,
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Best Local S
Matches 422
             Submitted (JUN-2001) to the EMBL/GenBank/DI
EMBL; AB06425; BAB83501.2; -.

MGD; MGI:1889272; Byff4.

GO; GO:0045202; C:synaptic junction; IDA.
GO; GO:0045202; C:synaptic vesicle; IDA.
GO; GO:0016347; F:calcium-independent cell
GO; GO:000515; F:protein binding; IPI.
GO; GO:0007115; P:cell adhesion; IDA.
GO; GO:007710; P:synaptogenesis; IDA.
GO; GO:00741; P:synaptogenesis; IDA.
GO; GO:00741; P:synaptogenesis; IDA.
GO; GO:000741; P:synaptogenesis; IDA.
GO; GO:000741; P:synaptogenesis; IDA.
SINTEPPO; IPRO03598; Ig-C2.
InterPro; IPRO03598; Ig-C2.
InterPro; IPRO03585; Neurexin-like.
Pfam; PF00047; 19; 3.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.

RROSITE; PS50335; IG_LIKE; 3.
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Q8R5MB;
01-JUN-2002
01-JUN-2002
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
 Immunoglobulin
SEQUENCE 456
                                                                                                                                                                                                                                                                                                                                                   Momoi T.;
"Biological function
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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Rodentia;
   49787 MW;
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Last ann
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Pred. No. 1.6e
1; Mismatches
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Sciurognathi; Muridae;
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1.6e-177;
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; Murinae; Mus
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Mus.

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78 120

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Query Match

Best Local Similarity

Matches 417; Conser
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Best Local Similarity
Matches 422; Conserv
                                                     01-JUN-2001
01-JUN-2001
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                   Q9BY67;
                                                                                                                                                                                                        SEQUENCE FROM N.A.
Zhou Y., Du G., Chen J., Yua
"Cloning of a novel human cD
superfamily.",
Submitted (MAR-1999) to the
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                  Nectin-like protein NECL2.
                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
[1]
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DE Nectin-like molecule 2.
CS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chorda
OC Mammalia; Eutheria; Rodent
OX NCELTAXID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Bra
RA Shingai T., Ikeda W., Kaku
RA Satoh K., Takeuchi M., Ima
RT "Implications of nectin-li
RT 2/IGSF4/RA175/SgIGSF/TSLC1
RT transmembrane protein loca
RL J Biol. Chem. 0:00 (2003)
DR EMBL; AY351388; AA002381.1
SQ SEQUENCE 417 AA; 45779
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                                                                                                                                                              Query Match 92.3%;
Best Local Similarity 93.4%;
Matches 395; Conservative
                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISUE=Brain;
STRAIN=C57BL/6; TISUE=Brain;
STRAIN=C57BL/6; TISUE=Brain;
STRAIN=C57BL/6; TISUE=Brain;
Shingai T., Ikeda W., Kakunaga S., Morimoto K.
Shingai T., Ikeda W., Kakunaga S., Morimoto K.
Shingai T., Ikeda W., Kakunaga S., Morimoto K.
Satoh K., Takeuchi M., Imai T., Monden M., Tak
"Implications of nectin-like molecule
2/IGSP4/RAI75/SgIGSF/TSLC1/SynCAM1 in cell-cel
transmembrane protein localization in epitheli
J. Biol. Chem. 0:0-0/2003)
EMBL; AY351388; AAQ02381.1; -.
SEQUENCE 417 AA; 45779 MW; 98500180D37845C
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Pred. No. 1.8e-163;
0; Mismatches 0;
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Sciurognathi; Muridae;
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Matches 394
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Saito K., Yamamoro J., Wakamatsu A., Nagai T., Ni
Nagahari K., Sugano S., Isogai T.;
"HRI human cDNA sequencing project.";
submitted (MAR-2002) to the EMBL/GenBank/DDBJ dai
EMBL; AK075502; BAC11657.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig.
InterPro; IPR003199; Ig.
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OBN2F4;

OBN2F4;

O1-OCT-2002 (TrEMBLrel. 22, Created)

O1-OCT-2002 (TrEMBLrel. 25, Last sequence update)

O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Hypothetical protein HEMBA1001879.

Homo sapiens (Human).

Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Eukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 3.

SMART; SM00409; IG; 3.

SMART; SM00408; IGC2; 3.

PROSITE; PS50835; IG_LIKE; 3.

Hypothetical protein; Immunoglo
SEQUENCE 443 AA; 48648 MW;
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                                                                            YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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  EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                  YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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                                                                                                                                                 IDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM
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48648 MW; 046B43AA156F6
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Pred. No. 6.9e-163;
5; Mismatches 24;
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A., Nagai T.,
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RX MEDININE=21085660; PubMed=11217951;

RX MEDININE=21085660; PubMed=11217951;

RX Mawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,

RA Arakawa T., Shinagawa M., Nishi K., Riyosawa H., Kondo S., Yamanaka I.,

RA Arakawa T., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Rieischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Gariboldi M.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.,
             Query Match
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EMBL; AK013775; BAB28988.1; -.

MGD; MGI:1889272; Igsf4.

GO; GO:0045202; C:synaptic junct:
GO; GO:0016347; F:calcium-indeper
GO; GO:0007155; P:protein binding
GO; GO:0007145; P:synaptogenesis;
GO; GO:0007416; P:synaptogenesis;
                                                                                                                                                                                                                                                                                              GO; GO:0045202; C:synaptic junction; IDA.
GO; GO:0009021; C:synaptic vesicle; IDA.
GO; GO:0016347; F:calcium independent cell i
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:0007116; P:synaptiogenesis; IDA.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
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Q1-JUN-2001 (TrEMBLrel. 17, I
Q1-CCT-2003 (TrEMBLrel. 25, I
2900073GO6Rik protein.
IGSF4 OR 2900073GO6RIK.
                                                                                                                                   Pfam; PF00047; 19; 3.
SMART; SM00408; IGC2; 1.
SMART; SS0035; IG_LIKE; 3
Immunoglobulin domain.
SEQUENCE 336 AA; 37157 MW
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Mammalia; Eutheria;
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74.2%; Score 1631; DB 11; ilarity 100.0%; Pred. No. 5.3e-130; Conservative 0; Mismatchen
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Best Local S
Matches 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=(578L/6; TISSUE=Spleen cell-derived;
ITO A., Koma Y., Nagano T.;
"A secretion form of SgIGSF/TSLC1.";
"A secretion form of SgIGSF/TSLC1.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ dat
EMBL; AB09241; BAC66173.1; -.

InterPro; IPR003599; Ig.
InterPro; IPR003199; Ig-21.

InterPro; IPR003599; Ig-c2.

Pfam; PF00047; ig; 3.

SMART; SM00409; IG; 3.

SMART; SM00409; IG; 3.

SMART; SM00409; IG; 3.

PROSITE; PS50835; IG_LIKE; 3.

SEQUENCE 336 AA; 37155 MW; 9EF3D8BBBE5EBF72 (
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01-JUN-2003
01-JUN-2003
01-OCT-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
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1-JUN-2003 (TrEMBLrel. 24, Last seq
1-CCT-2003 (TrEMBLrel. 25, Last ann
secretion form of SgIGSF/TSLC1.
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313; Conserv
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                             TTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                        TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
                                                                                                                                                                                PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                                                                                                                                           PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDDPQESYTTI
YTVTSQLMLKVHKEDDGVÞVÍCQVEHÞAVTGNLQTQRYLEVQYKÞQVHIQMTYÞLQGLTR
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                                                                                                                                                                                                                                                                                                                                                                      74.2%; Score 1631; DB 11; 100.0%; Pred. No. 5.3e-130; ive 0; Mismatches 0;
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RESULT 10
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ID Q9Z2H
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ITO A., KOMB Y., Nagano T.;

ITO A., KOMB Y., Nagano T.;

"Cloning of a secretory isoform of submitted (OCT-2002) to the EMBL/G EMBL, AB094146; BAC66178 1; --

Interpro; IPR003599; Ig.

Interpro; IPR003599; Ig.-like.

Interpro; IPR003599; Ig.-c2.

Pfam; PF00047; ig; 3.

Pfam; PF00047; ig; 3.

R SMART; SM00409; IG; 3.

R SMART; SM00409; IG; 3.

R PROSITE; PS50835; IG_LIKE; 3.

R PROSITE; PS50835; IG_LIKE; 3.

R SEQUENCE 333 AA; 36915 MW; D.
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Best Local Similarity
Matches 310; Conserv
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Q86WB8;
01-JUN-2003
01-JUN-2003
01-OCT-2003
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Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secretory isoform STSLC-1.
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Metazoa; Chordata; C
---heria; Primates; (
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Pred. No. 1.2e-128;
0; Mismatches 3;
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Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
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Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Zhou Y., Apolizo, a novel cDNA encoding a member of imm
Submitted (APR-1998) to the EMBL/GenBank/DDBJ day
EMBL, Apolizo, AAC67243.1;
Zhou J., Apolizo, AAC67243.1;
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Q9QYL4;
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01-MAY-2000 (TrEMBLrel. 1
01-OCT-2003 (TrEMBLrel. 2
Adhesion protein RA175C.
IGSF4 OR RA175C.
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01-OCT-2003
Nectin-like
                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI TaxID=10090;
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SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE;
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Mammalia; Eutheria;
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SEQUENCE 295
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003585; Neurexin-like.
                                Soyama
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                                                              SEQUENCE FROM N.A.
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                                Fujita
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Rodentia;
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Rodentia;
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Pred. No. 7.2e-123;
                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                               Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                Mukasa
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annotation update)
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Murinae; Mus
                                      Momoi
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Best Local S
Matches 291
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GO; GO:0008021; C:synaptic vesicle; IDA.
GO; GO:0008021; C:synaptic vesicle; IDA.
GO:0005015; F:structein binding; IPI.
GO:0005015; F:protein binding; IPI.
GO:GO:0007115; P:cell adhesion; IDA.
GO:GO:0007415; P:synaptogenesis; IDA.
InterPro; IPR003110; Ig-like.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003598; Neurexin-like.
Pfam; PF00047; ig; 2.
SWART; SW00204; 4.1m; 1.
SWART; SW00408; IGC2; 1.
SWART; SW00408; IGC2; 1.
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Immunoglobulin
SEQUENCE 306
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Q9QYL6;
01-MAY-2000
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Submitted
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                                                                                                                         Momoi T.; "RA175, a
                                                                                                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                         Mammalia; Eutheri
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                              Adhesion protein
IGSF4 OR RA175A.
                                                                                                                                                                 Soyama
                                                                                                                                                                                      SEQUENCE
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MGI:1889272; Igsf4. ---
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A., Fujita
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Rodentia;
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25,
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Last seq
Last ann
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EMBL/GenBank/DDBJ dat
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                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
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; Murinae; Mus.
          molecule
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          IDA.
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Best Local Simi
Matches 284;
    NAMEL 1. PRODUCT 1. SUBMITTED TO SPECIFIC adhesion prot Submitted (DEC-1998) to the EMBL/GenBank/DDBJ EMBL, ABO21965; BAA87915.1; -.

MGD; MGI:1889272; Igsf4.

GO; GO:00045202; C:synaptic junction; IDA.

GO; GO:0016347; F:calcium-independent cell add

GO; GO:0016347; F:calcium-independent cell add

GO; GO:0005515; F:protein binding; IPI.

GO; GO:0007155; P:cell adhesion; IDA.

InterPro; IPR00310; Ig-like.

InterPro; IPR003598; Ig_C2.

InterPro; IPR003585; Neurexin-like.

PFGAM; PF00047; ig; 2.

SWART; SW00294; 4.1m; 1.

SWART; SW00408; IGC2; 1.

PROSITE; PF50835; IG_LIKE; 2.
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InterPro; IPRO03598; Ig-c2.
InterPro; IPR003598; Neurexin-like.
Pfam; PF00047; ig; 2.
SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGc2; 1.
SMART; PS50935; IG LIKE; 2.
Immunoglobulin domain.
SEQUENCE 295 AA; 32347 MW; FDD9E
                                                                                                                                                                                                                                                        Adhesac.
IGSF4 OR RA1755.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                    Soyama
                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2003 (TrEMBLrel. 25,
Adhesion protein RAI75B.
IGSF4 OR RAI75B.
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                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                             Momoi T.;
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GO:0007155; P:cell adhesion; IDA.
GO:0077416; P:synaptogenesis; IDA.
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EMBL/GenBank/DDBJ dat
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Pred. No. 2.3e-
2; Mismatches
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                                                                                                                                                                                                                     Mukasa
                                                                                                                                                                                                                                                                                                                                                                          289
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RESULT 14
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AC Q90YL3
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WRA175, a novel neuron specific adhesion protein.";

L Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databa
R MBL; AB021967; BAA87917.1; -.

R MGD; MGJ:1889272; Igsf4.

R GO; GO:0045302; C:synaptic junction; IDA.
R GO; GO:000501; C:synaptic vesicle; IDA.
R GO; GO:000501; C:synaptic vesicle; IDA.
R GO; GO:0016347; F:calcium-independent cell adhesion
R GO; GO:0005515; F:protein binding; IDA.
R GO; GO:0007515; F:cell adhesion; IDA.
R GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR003158; Ig-like.
InterPro; IPR003158; Ig-like.
InterPro; IPR003158; Meurexin-like.
Pfam; PF00047; Ig; 2.

Pfam; PF00047; Ig; 2.

Pfam; PF00047; Ig; 2.
                                                                                                                                   Query Match
Best Local S
Matches 267
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IGSF4 OR RA175N.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 2.
SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGc2; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                            Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Soyama A., Fujita E., Urase K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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    190
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                                                                                                                                   al Similarity
267; Conserv
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272; Conser
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                                                                          MIDIOXDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML
KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTC
                                             MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYF
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                                                                                                                                   62.8%; llarity 90.8%; Conservative
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Pred. No. 7.9e
2; Mismatches
                                                                                                                                   Score 1380.5; DB 1:
Pred. No. 7.4e-109;
2; Mismatches 8;
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                                                                                                                                                                                                                            A295F4DEA2724B04 CRC64;
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                                                                                                                                                                            DB 11; Length
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Best Local S
Matches 192
                                                                                                                                                                                                                                                                                                                                                                                                             Kochrer K., Beyer A., Mewes H.W., Weil B., Wiemann S.;
L. Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
R. EMBL; AL834270; CAD38945.1; -.
R. InterPro; IPR003599; Ig.
R. InterPro; IPR007110; Ig-like.
R. InterPro; IPR007110; Ig-like.
R. InterPro; IPR007110; Ig-like.
R. InterPro; IPR007110; Ig-like.
R. Ffam; PF00047; 1g; 3.
R. SMART; SM00409; IG; 2.
R. SMART; SM00409; IG; 2.
R. SMART; SM00408; IGC2; 2.
R. SMART; SM00408; IGC2; 2.
R. SMART; SM00408; IGC2; 2.
R. SMART; PS50835; IG LIKE; 3.
R. Hypothetical protein; Immunoglobulin domain.
SEQUENCE 435 AA; 47554 MW; 59DDD41B7F34D446 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRN3J6 PRELIMINARY; PRT; 435 AA.
QRN3J6;
QL-OCT-2002 (TrEMBLrel. 22, Created)
QL-OCT-2003 (TrEMBLrel. 22, Last sequence update)
QL-OCT-2003 (TrEMBLrel. 25, Last annotation update)
QL-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
DKF2P761c128.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Amygdala;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224
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   305
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                                                                                                                                                                                                          130
                                                                                                                                                                                                                                                                                                                                                        tch 40.8%; Score 897; DB 4; Length 435; al Similarity 44.2%; Pred. No. 1.5e-67; 192; Conservative 75; Mismatches 139; Indels
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                            ELTCEAIGKPQPVMVTWVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGK
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                                                             ILTCESKGKPLPEPVLWTKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCEATNTIGO
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Search completed: July Job time : 60.1711 secs 7, 2004, 06:02:45

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7: geneseqp2003bs:*
8: geneseqp2004s:*
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Abr92181	Abo16281	Abr98758		30450			89368	Abu91675	Abu97969	98754	44	50240	Abr94621	Abr74859	Abo02705	ω	76	Abu96145	Abr68092	
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ALIGNMENTS

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(first entry)

Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; 37-1; 87-1; T cell proliferation; natural killer cell; NK; tumour cell; biological activity; quality control reagent; treatment; inflammation; immune system disorder; autoimmune; viral infection; infectious disease; organ transplant rejection; bone marrow; modulator; immune response. 17-FEB-2000. Modified-site Modified-site Modified-site Mouse lymphoid derived dendritic cell adhesion molecule. 05-AUG-1999; WO200008158-A2 Modified-site Modified-site Modified-site 98US-0095672P. 99WO-US017905 378. .423 /label= Cy /labsob /labsob /labsob 49..51 /note= "N-Glycosylation site" /note= 357. .3 290. .292 286. .288 /note= "N-Glycosylation site"
147. .149 83. .85 Location/Qualifiers /note= note= note= label= . 97 = "N-Glycosylation site"
.377 "N-Glycosylation site" "N-Glycosylation site" "N-Glycosylation site" Transmembrane_domain Cytoplasmic_domain

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Matches 423
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                                                standard; protein;
                                                                                                                                                                                             GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK
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Pred. No. 1.
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1.8e-151;
es 0;
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21-NOV-2000
Protein encoded by human secreted protein gene
                               (first
                               entry)
    #11.
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Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder, Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human.

WO200029435-A1

25-MAY-2000

27-OCT-1999; 99WO-US025031

28-OCT-1998; 98US-0105971P

(HUMA-) HUMAN GENOME SCI INC

Greene Ruben XX. Olsen HS, Young PE, Kenny JJ, Moore PA, Wei K

WPI; 2000-387742/33

Isolated nucleic acid molecules encoding human secreted protein for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, wounds, and infectious diseases. proteins are used cancer,

Disclosure; Page 182-183; 803pp; English

The present invention relates to 12 secreted human proteins and the current control of the present invention relates to 12 secreted provide sequences given in AAA80606-A80623 encode the 12 secreted protein sequences given in CC AAA80606-A80623 encode the 12 secreted protein sequences given in CC dependent on the tissues in which they are expressed. Examples of the cactivities of the proteins include: immunosuppressant; anti-inflammatory; anti-arthritic; antirheumatic, dermatological; antiproliferative; antiarreriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antiarreriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antiagonists may be used to treat prevent and/or diagnose various disease, antagonists may be used to treat prevent and/or diagnose various disease, and sorders and conditions examples of which include: immune disorders e.g. Addison's disease, rheumatoid arthritis, dermatitis, and multiple colarosis; inflammatory disorders e.g. inflammatory bowel disease, coronary disorders e.g. inflammatory bowel disease, coronary coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing the proteins and coronary and coronary and coronary and coronary are disorders e.g. inflammatory bewel disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and polymphoma. The proteins and polymucleotide sequences may also be used in wound healing the following the proteins and polynucleotide sequences may also be used in wound heali and the treatment of infectious diseases. The human secreted protein #11 and protein sequences are represented in sequences AAA80616 and AAB25586. Sequences AAA80677-A80682 represent genes related to the protein gene#11

Sequence 442

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             PURQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                            AAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                           AAPPGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                       Conservative
                                                                                                98.7%;
                                                                                      Score 2169; DB 3;
Pred. No. 2.1e-149;
1; Mismatches 4;
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RESULT 3
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AAY9
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                                The present sequence is a novel human cell surface receptor protein (C) (HCSRP) designated HCSRP-8. The nucleotide sequence was identified in Incyte Clone 312256 from the CDNA library LUNNOTO2, which was made from CC RNA isolated from lung tissue. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to immuno-superfamily protein B12 g3779242. HCSRP and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRP. Such CC disorders include cancers such as leukaemia and melanoma, immune CC disorders such as rheumatoid archritts, asthma and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as CC akathesia, Alzheimer's disease, multiple sclerosis and epilepsy. CC polymucleotides encoding HSCRPs may be used as hybridisation probes to diagnose these conditions. Anti-HCSRP antibodies may be used as antagonists, as a targeting or delivery mechanism for bringing CC pharmaceutical agents into contact with cells or tissues expressing HCSRP and for diagnosis of HCSRP-related disorders. HCSRP and its catalytic or immunogenic fragments are useful for drug screening using libraries of
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07-DEC-1998;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                    Claim 1; Page 81-82;
                                                                                                                                                                                                                                                                                                                             New human cell surface receptor protein and polynucleotide useful for diagnosis, prevention and treatment of cancer, immune disorders, infection and neuronal disorders.
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cc cell addesion molecule, LDCAM. It is found on lymphoid derived dendritic cc cells and displays homology to adhesion molecules, B7-11 and cytoplasmic cregion of B7-11. Human LDCAM is expressed in breast, retina, foetal cliver, spleen and heart, lung, muscle, placenta, thyroid and lung carcinoma. LDCAM polypeptides interacts with T cell surface molecules to carcinoma. LDCAM polypeptides interacts with T cell surface molecules to carcinoma. LDCAM polypeptides interacts with T cell surface molecules to carcinoma. LDCAM binding protein and increases natural killer (NK) cc and B7-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and cas quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, clisammation, autoimmune disorders, viral infected cells, infectious clisamention or reducing the effect of organ and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or
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N-PSDB;
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밁 Ş Ś В Ś á 맑 S 片 В 361 319 301 259 199 139 421 379 241 181 121 EYF GVVAVVVFAMI.CILIIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI YTVTSQLMLKVHKEDDGVPVICQVEHÞAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIG EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 423 318 300 258 240 198 360

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                                                                                                                                                                                                                                                                                                                                         New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
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Zhao
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ilan; immunostimulant; cytostatic; immunosuppressive;
antiallergic; gene therapy; wound healing; tissue rinervous system disorder; Alzheimer's disease;
ilsease; Huntington's disease; immune disorder;
sorder; multiple sclerosis; diabetes; allergy.
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The invention relates to an isolated polynucleotide (I) comprising one 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the prote (II) encoded by (I) (ABF62809-ABP63053) or an antibody (III) to (II). (II) and (III) are useful for diagnostic evaluation of disorders. (I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healiand tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral

he protein (II).

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Claim 20;

SEQ ID NO 262; 284pp + Sequence Listing;

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Matches 418
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19-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                cytostatic; antiinflammatory; immunomodulator; neuroprotective; hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive;
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Pred. No. 2.1e-149;
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CC encoding secreted proteins or a polynuclectide fragment of the cDNA contained in the specification, its species homologue, a variant No. CC defined in the specification, its species homologue, a variant No. CC defined in the specification, its species homologue, a variant No. CC defined in the polynuclectide having a polynuclectide capable of contained in the polynuclectide having a polynuclectide capable of contained the polynuclectide capable of contained the polynuclectide capable of contained the polynuclectide capable of contained the polynuclectide capable of contained the polynuclectide secreted polypeptide fragment, domain, epitope, the contained are combinant vectors, host cells (for producing the polypeptide), the contained polypeptide fragment, domain, epitope, full-length contained to a polypeptide fragment, domain, epitope, full-length contained to a polypeptide fragment, domain, epitope, full-length contained to the polypeptides, diagnosing, treating, preventing contained a medical condition by administering the polymucleotide or the polypeptide, the gene corresponding to the cDNA sequence and contained the polypeptides, diagnosing, treating an activity in a biological assay (by expressing the cDNA sequence in a biological assay (by expressing the cDNA sequence and contained the polypeptides, nucleic acids and antibodies are useful for disorders, neurological and blood clotting disorders (many examples are contained to a contained the supernature and the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernature and contained the supernatur
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01-NOV-2001;
26-NOV-2001;
The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates
                                                                                                                                        Claim
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(FARB )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the expression of a polynucleotide sequence which is differentially cexpressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic construction cinjury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human procein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed construction specification, but was obtained in electronic form directly from WIPO at fig. wipo.int/pub/published_pct_sequences.
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Novel human secreted protein #11 associated protein

secreted protein; cancer; liver disorder; hepatitis; disorder; Alzheimer's disease.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule, useful for preparing preventing, treating or ameliorating a medical cliver disorders or neural disorders.
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                                       GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKK
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                         GVVAVVVFAMLCLLI I LGRYFARHKGTYFTHEAKGADDAADADTAI I NAEGGQNNSEEKK
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cc modulating agent, by contacting an assay system computating appurising a purified HM cc polypeptide (human orthologue of genes that modify the p53 pathway in cc prosphila) or nuclaic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference cc activity, and detecting a test agent biased activity of the assay system. CC Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator ct hat specifically binds to a HM polypeptide comprising an HM amino acid comparising contacting the patient (comprising contacting the cell with a patient (comprising contacting the cell with a patient (comprising contacting the cell with a p53 pathway cf a disease in a patient (comprising; (a) obtaining a biological sample cf rum the patient; (b) contacting the sample with a probe for HM contacting the comparising in a control; and (d) determining contentified by (M1) are useful hood disease). (M1) is useful condentified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as angiogenesis, apoptotic or cell proliferation of the cell, so that the cell with sequences (condentified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in a variety of diagnostic or cell contified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in a variety of diagnostic and contified by (M1) are useful in the cell contified and contified by (M
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lung cancer; ovarian cancer; angiogenesis; cell cycle;
apoptotic disorder; cell prolliferation disorder.
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antiapoptotic; p53 pathway; breast
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WPI; 2003-156859/15
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2001US-0328605P.
2002US-0357253P.
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              Francis-Lang H,
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       GVVAVVVEAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGQNNSEEKK
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N-PSDB; ACD13404.

Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.

Example 2; Page 557-559; 678pp; English

The invention relates to identifying (MI) a candidate p53 pathway combating agent, by contacting an assay system comprising a purified HM copolypeptide (human orthologue of genes that modify the p53 pathway in cosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference cactivity, and detecting a test agent, the system provides a reference cactivity, and detecting a test agent with a candidate modulator contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid contacting a specifically binds to a HM polypeptide comprising (M3) a p53 pathway of a disease in a patient (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising contacting the sample with a probe for HM comparison indicates a likelihood disease). (M1) is useful for identifying modulators of the p53 pathway. A probe for HM expression is useful for identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to defects in the p53 pathway, such as, angiogenesis, apoptotic or cell proliferation of the cell, so that the cell undergoes normal (M2) and (M3) are useful for treating defects in the p53 pathway of a cell, thus restoring cells proposed to cell proliferation disorders. The present sequence

Similarity GVVAVVVFAMLCILI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGQNNSEEKK TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR PNROTIYERDERPLKDSREQLLNESSSELKVSLTNVSISDEGRYECQLYTDPPQESYTTI PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI AAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN AAPPGLRLRLLLLLSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVIQLLN EGDALELT CEATGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR TVLVPPRNLMIDIQRDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM Conservative MLYVYDPPTTIPPPTTTTTTTTTTTLTIITISRAGEEGSIRAVDHAVIG 98.6%; 2; Score 2166; DB 6; Pred. No. 3.4e-149; 2; Mismatches 4; Length 442; <u>.</u> Gaps 180 138 420 378 360 300 258 240 198 78

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                                                                                  The invention discloses a composition comprising two or more isolated rat CC or human polynucleotides or a polynucleotide which represents a fragment, CC derivative or allelic variation of the nucleic acid sequence. Also CC claimed are a vector comprising the novel polynucleotide, a host cell CC comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a CC that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially composition of the polynucleotide sequence which is differentially composition and a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound to result an animal of one or more of the polypeptides given in the general part of the polypeptides or their antibodies. The polynucleotide or the compound that composition and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that composition and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that composition and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that composition and a pharmaceutical composition composition and composition of the polypeptides or their antibodies. The polynucleotide or the compound that composition and composition and composition and composition and composition and composition and composition and composition and composition and composition and composition and composition and composition and compositi
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01-NOV-2001;
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                                                                specification, but was obtained.int/pub/published
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segmental nerve injury; chronic constriction injury;
nerve injury; SNI; Chung.
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Best Local Similarity
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01-NOV-2001;
26-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
New composition comprising
                                              GENBANK; AAF69029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claimed are a vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a comparising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a compound that is differentially expressed in neuronal tissue of a first animal compound that is differentially expressed in neuronal tissue of a first animal compound that regulates the expression of the polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound which regulates the compound or small molecule that regulates the extivity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a contivity in an animal of one or more of the polypoptides given in the computed for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more or more of polypoptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene conjury in a pain animal (e.g. gene conjury conjuration) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed confuring to the printed confuring pain. Note: the sequence data for this patent did not form part of the printed confuring pain. State of the printed confuring pain with the specification, but was obtained in electronic form directly from wipo at the printed confuring pain and confuring pain.
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18-DEC-1997;
05-JAN-1998;
09-FEB-1998;
09-FEB-1998;
                                                                                                                                                                                                                          The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes are
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12-DEC-1997;
                                                                                                                                                                    Sequence
                                                                                                                                                                                        identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
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                                            PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                      AAPPGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                              PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                           AAPPG--LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDSVIQLLN
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Pred. No. 5.8e-148;
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TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mbrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO241; PRO353; PRO299; PRO233; PRO344; PRO347; PRO355; PRO353; PRO365; transmembrane polypeptide; antibody; screening; on; inhibition; probe; primer; human.
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Matches 416;
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16-DEC-1998;
22-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                 New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant recording interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 440
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Hillan KJ,
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  GVVAVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK
                                                       VGKAHSDYMLYVYDPETTIFPETTITITTTTTTTTILTIITDSRAGEEGIIGAVDHAVIG
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ME, Goddard I
Kljavin IJ,
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ilarity 98.3%;
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d A, Godowski
J, Napier MA,
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i PJ, Grimaldi CJ, Gu
, Roy MA, Tumas D, V
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

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       9 US-09-778-510-22

9 US-09-778-107B-4

14 US-10-302-041-22

15 US-10-015-115-113

15 US-10-015-115-113

9 US-09-778-187B-2

10 US-09-778-187B-2

10 US-09-984-130-136

10 US-09-984-130-136

12 US-10-363-616-262

14 US-10-363-615-262

14 US-10-303-041-20

15 US-10-015-115-111

15 US-10-015-115-111
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Sequence 22, Appli
Sequence 4, Appli
Sequence 22, Appli
Sequence 112, App
Sequence 113, App
Sequence 20, Appl
Sequence 2, Appli
Sequence 136, App
Sequence 136, App
Sequence 262, Appl
Sequence 27, Appl
Sequence 11, Appl
Sequence 111, Appl
Sequence 111, Appl
Sequence 111, Appl
Sequence 61, Appl
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ALIGNMENTS

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FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: POT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
LENGTH: 423
TYPE: PRT
ORGANISH: Mus musculus
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APPLICANT:
Baum,
TITLE OF INVENTION:
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CURRENT APPLICATION NUMBER: US/09/778,1878
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: PCT/US99/17905
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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APPLICANT: Fanslow III, William C
TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILE REFERENCE: 2873-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 423
TYPE: PRT
ORGANISM: mus musculus
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                                                                                                                 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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GENERAL INFORMATION:

APPLICANT: Malyankar, Uriel N APPLICANT: Shenoy, Suresh G

Shenoy, Suresn & Spytek, Kimberly A Zerhusen, Bryan D

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

APPLICANT:

Gangolli, Esha A Shimkets, Richard A Patturajan, Meera Guo, Xiaojia Kekuda, Ramesha

Taupier, Raymond J

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PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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GVVAVVVFAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGQNNSEEKK
                                                                                                                                                                                EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
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                                    GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK
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                                                                                                                                                         EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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US-10-015-115-113
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CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-02-66
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 205
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 113
                                                                                                                                                                                                                                                                                                                                                            Matches 422;
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Best Local S
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/313,283 PRIOR FILING DATE: 2001-08-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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TYPE: PRT
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Kekuda, Ramesha
Gangolli, Esha A
Shimkets, Richard A
EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
                                                                      YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                     TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
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                                      YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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Spytek, Kimberly A
Zerhusen, Bryan D
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Patturajan, Meera
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5. US20030207800A1
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Pred. No. 6.26
1; Mismatches
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; TYPE: PRT ; ORGANISM: Mus musculus US-10-015-115-112

SOFTWARE: PatentIn Ver. SEQ ID NO 112

ENGTH:

445

PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17

E: 2001-08-17 NOS: 205

Best Local Similarity Matches 423; Conserv

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Query Match

APPLICANT: Li, Li
APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotide
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT FILING DATE: 2002-09-23
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR APPLICATION NUMBER: 60/309,261
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; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo s
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US-09-778-510-20
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Matches
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Best Local
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                          HYE
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                                                   GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK
                                                                                                               VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTILTIITDSRAGEEGTIGAVDHAVIG
                                                                                                                                                                     EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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                                                                                                                                                    EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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ilarity 98.8%;
Conservative
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  441
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Pred. No. 2.2e-168;
1; Mismatches 4;
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US-09-984-130-136
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FILE REFERENCE: 2873-US
CURRENT APPLICATION NUMBER: US/09/778,187B
CURRENT FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: PATOWERS PRIOR PRILING DATE: 1999-08-05
PRIOR PRILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 442
TYPE: PRT
ORGANISM: homo sapiens
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Best Local Simi
Matches 418;
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Patent No. US2002018712A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow III, William C
APPLICANT: MISSION MOLECULES DESIGNATED LDCAM
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EYF
                                                                     GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK
                                                                                          GVVAVVVFAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGQNNSEEKK
                                                                                                                                                               VGKAHSDYMLYVYDPPITIIPPPTTTTTTTTTTTTTILTIITDSRAGEEGTIGAVDHAVIG
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Pred. No. 2.2e-168;
1; Mismatches 4;
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Sequence 136, Application US/09984130
Publication No. US20030055231A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792

420

300

258

318

378

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PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION NUT/BER: 09/836,353
PRIOR APPLICATION NUT/BER: 60/198,407
PRIOR APPLICATION NUT/BER: 60/198,407
PRIOR PILING DATE: 2000-04-19
PRIOR PILING DATE: 2000-04-19
PRIOR PILING DATE: 1999-10-27
PRIOR PILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR PILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 136
LENGTH: 442
CURRENT APPLICATION NUMBER: US/09/836,353A
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/196,407
PRIOR FILING DATE: 2000-04-19
PRIOR PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR APPLICATION NUMBER: FO/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR APPLICATION NUMBER: 50/105,971
PRIOR PILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 136
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US-09-836-353A-136
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Publication No. US20030129685A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF489P1
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Best Local Similarity
Matches 418; Conserv
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98.8%;
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Pred. No. 2.2e-168;
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Sequence 262, Application US/10363616

Publication No. US30040044181A1

GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 2172-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 262
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-10-363-616-262
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; TYPE: PRT
; ORGANISM: Homo s
US-09-836-353A-136
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Pred. No. 2.2e-168;
1; Mismatches 4;
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Pred. No. 2.2e-168;
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APPLICANT: BAUM. Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION UMBER: US/10/302,041
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/99/778,510
PRIOR FILING DATE: 2001-02-07
PRIOR FILING DATE: PRIOR PRIOR PRIOR BAPPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-302-041-20
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US-10-302-041-20
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Best Local S
Matches 418
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                                                                     YTVTSQLMLKVHKEDDGVPV1CQVEHPAVTGNLQTQRYLEVQYKPQVH1QMTYPLQGLTR
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                                                    YTVTSQLMLKVHKEDDGVÞVÍCQVEHÞAVTGNLQTQRXLEVQYKÞQVHIQMTYÞLQGLTR
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98.8%;
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Pred. No. 2.2e-168;
1; Mismatches 4;
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Sequence 1, Application US/10403107

Publication No. US20030165974A1

GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MED APPLICANT: REEVES, Roger
APPLICANT: YOSHINGEL, Muramaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-
FILE REFERENCE: JHU1770-1

CURRENT APPLICATION NUMBER: US/10/403,107

CURRENT FILING DATE: 2003-03-28

PRIOR APPLICATION NUMBER: US/09/930,803

PRIOR REPLICATION NUMBER: US/09/930,803

PRIOR REPLICATION NUMBER: US/09/930,803

PRIOR REPLICATION NUMBER: US/09/930,803

PRIOR REPLICATION NUMBER: US/09/930,803

PRIOR FILING DATE: 2001-08-15

SOFTWARE: PATENTIAL DATE: 2001-08-15

SOFTWARE: PATENTIAL DATE: 32

SOFTWARE: PATENTIAL DATE: 32

SOFTWARE: PATENTIAL DATE: 32

TENGTH: 442

TYPE: PRI
GRANISM: Homo sapiens
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Best Local Similarity 98.8%;
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Pred. No. 2.2e-168;
1; Mismatches 4;
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RESULT 13

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APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Enc.
TITLE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR PRILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-02
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR APPLICATION NUMBER: 60/313,283
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; ORGANISM: Homo sapiens
US-10-015-115-111
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APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Eryan D
APPLICANT: Zerhusen, Meera
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Best Local
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Publication No. US20030207800A1
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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SOFTWARE: PatentIn Ver.
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Gangolli, Esha A
Shimkets, Richard A
Taupier, Raymond J
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NOS: 205
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Pred. No. 2.2e-168;
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Publication No.

GENERAL INFORMATION:

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APPLICANT: Malyankar, Uriel M

APPLICANT: Shenoy, Suresh G

APPLICANT: Spytek, Kimberly A

Porticant: Zerhusen, Bryan D

Porticant: Zerhusen, Meera
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TITLE OF INVENTION: Proteins, Polymucleotides Enc
TITLE OF INVENTION: Using the Same
FILE REPERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-16
PRIOR PRIOR DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR PILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR PILING DATE: 2001-07-10
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Best Local Sim
Matches 417;
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SEQ ID NO 110
LENGTH: 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/313,283
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: Patentin Ver. 2.1
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YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                       TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
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Gangolli, Esha A
Shimkets, Richard A
Taupier, Raymond J
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Li, Li
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Pred. No. 3.9e-168;
2; Mismatches 4;
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-028-61 -028-61 -0128020158309A1 INFORMATION: ANT: Baker, Kevin ANT: Bottetain, David ANT: Betcain, Mapoleone ANT: Ferrara, Napoleone ANT: Gerritsen, Mary ANT: Goddard, Audrey ANT: Goddard, Audrey ANT: Godwaki, Paul ANT: Godwaki, Paul ANT: Godwaki, Paul ANT: Hillan, Kenneth ANT: Mapier, Mary ANT: Hillan, Kenneth ANT: Tumas, Daniel ANT: Mood, William DF INVENTION: SECRETED AND TRANSMEMBRA DF INVENTION: ACIDS ENCODING THE SAME EFFRENCE: P2548F1C1 FILING DATE: 2001-05-25 FILING DATE: 2001-05-25 FILING DATE: 2001-05-25 FILING DATE: 2001-05-25 FILING DATE: 39.3%; Score 2149; A16; Conservative 1; Mismatches 1 AAPPGLEATILILLIAAAALIPTGDGQNLFTKG 1 DAPPGL-LRILLILLSAAALIPTGDGQNLFTKG 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSI 1	LOGLTR	81 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNI
Jon US/098660 Jaoyal Javid Javid Jandrey Jean Jaret Jistin Genneth Jistin Genneth Jistin AGIDS ENCODI NUMBER: US/09 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 12 2001-05-25 13 2001-05-25 14 removed 15 2001-05-25 15 2001-05-25 16 2001-05-25 17 2001-05-25 18 2001-05-25	TINVSISDEGRYFCQLYIDPPQESYTTI	61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSI
ion US/09866028 3309A1 3309A1 n, David n, David n, David n, David n, Mapoleone f. Ellen en, Mary nary nary nary location for an an an an an an an an an an an an an	Indels 2; Gaps ATISCQVNKSDDSVIQLLN ATISCQVNKSDDSVIQLLN	I Similarity 98.3%; Pr 416; Conservative 1; 1 AAPPGLELELLELAAALIF 1 AAPPGERLILLESAAALIP
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	TAIINAEGGQNNSEEKK TAIINAEGGQNNSEEKK	79
361 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK	RAGEEGTIGAVDHAVIG : RAGEEGSIRAVDHAVIG	301 VGKAHSDYMLYVYDÞÞTTIÞÞÞTTTTTTTTTTTILTIITDSRAGBEGTIGAVDHAVI
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Qy 421 EYF 423 Db 437 EYF 439			
``	361 GVVAVVVFAMLCILIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 420 	301 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTILTIITDSRAGEEGTIGAVDHAVIG 360	241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300

Search completed: July 7, 2004, 06:39:09 Job time: 607.382 secs

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